

OM protein - protein search, using SW model
Run on: August 28, 2006, 17:25:54 ; Search time 196 Seconds
(w/o alignments)
620,508 Million cell updates/sec

Title: US-10-006-867-2
Perfect score: 1392
Sequence: 1 MWWFQQGSLFLPSALVIWTS.....YDTAPCPINNERTRLLSRDI 266
Scoring table: BLOSUM62

Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 1500 summaries

A_Geneseq_8:
1: geneseqP19808;*
2: geneseqP19808;*
3: geneseqP20018;*
4: geneseqP20018;*
5: geneseqP20028;*
6: geneseqP20038;*
7: geneseqP20038;*
8: geneseqP20048;*
9: geneseqP20048;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description	Description
RESULT 1	ID AAY66636	Standard; protein;	266	AA.			
	DB Membrane-bound protein PRO180.						
	PN WO9963108-A2.						
	PD 09-DEC-1999.						
	PA (GETH) GENENTECH INC.						
	Query Match	100.0%		Score 1392;	DB 3;	Length 266;	
	Best Local Similarity	100.0%		Pred. No.	5e-149;		
RESULT 2	ID AAU29028	Standard; protein;	266	AA.			
	DB Human PRO polypeptide sequence #5.						
	PN WO200168848-A2.						
	PD 20-SEP-2001.						
	PA (GETH) GENENTECH INC.						
	Query Match	100.0%		Score 1392;	DB 4;	Length 266;	
	Best Local Similarity	100.0%		Pred. No.	5e-149;		
RESULT 3	ID AAM39568	Standard; protein;	266	AA.			
	DB Human polypeptide SEQ ID NO 2713.						
	PN WO200153312-A1.						
	PD 26-JUL-2001.						
	PA (HYSE-) HYSEQ INC.						
	Query Match	100.0%		Score 1392;	DB 4;	Length 266;	
	Best Local Similarity	100.0%		Pred. No.	5e-149;		
RESULT 4	ID AAB65159	Standard; protein;	266	AA.			
	DE Human PRO180 (UNQ154) protein sequence SEQ ID NO:23.						
	PN WO20073454-A1.						
	PD 07-DEC-2000.						
	PA (GETH) GENENTECH INC.						
	Query Match	100.0%		Score 1392;	DB 4;	Length 266;	
	Best Local Similarity	100.0%		Pred. No.	5e-149;		
RESULT 5	ID ABB9038	Standard; protein;	266	AA.			
	DE Human polypeptide SEQ ID NO 2714.						
	PN WO200190304-A2.						
	PD 29-NOV-2001.						
	PA (HUMA-HUMAN GENOME SCI INC.						
	Query Match	100.0%		Score 1392;	DB 5;	Length 266;	
	Best Local Similarity	100.0%		Pred. No.	5e-149;		
RESULT 6	ID AbG95851	Standard; protein;	266	AA.			
	DE Human secreted/transmembrane protein PRO180.						

PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 5; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 7
ID ABUS8404 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 8
ID ABUB7952 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 9
ID ABUB3267 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 10
ID ABR66141 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180. SEQ ID NO:10.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 11
ID ABR65531 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180. SEQ ID NO:10.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 12
ID ABU99471 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 13
ID ABU57974 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 14
ID ABU59052 standard; protein; 266 AA.
DE Novel human secreted or transmembrane protein PRO180.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 15
ID ABU2364 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 16
ID ABU82710 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032113-A1.

PPD	13-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	17	ID	ABU89831	standard; protein; 266 AA.			
	DE	Novel human secreted and transmembrane protein PRO180.					
	PN	US2003036147-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	18	ID	ABR68080	standard; protein; 266 AA.			
	DE	Human secreted polypeptide PRO180,	SEQ ID NO:10.				
	PN	US2003027264-A1.					
PPD	06-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	19	ID	ADA57044	standard; protein; 266 AA.			
	DE	Human secreted protein #327.					
	PN	WO200202994-A2.					
PPD	27-DEC-2002.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	PA	(HUMA-) HUMAN GENOME SCI INC.					
	DE	Novel human secreted/transmembrane protein, #9.					
	PN	US2002160384-A1.					
RESULT	20	ID	ABU60493	standard; protein; 266 AA.			
	DE	Human secreted/transmembrane protein.	#9.				
	PN	US2003036144-A1.					
PPD	31-OCT-2002.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	21	ID	ABU96133	standard; protein; 266 AA.			
	DE	Novel human secreted and transmembrane protein PRO180.					
	PN	US2002160384-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	22	ID	ABU92564	standard; protein; 266 AA.			
	DE	Human secreted/transmembrane protein (PRO) #5.					
	PN	US2003036149-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	23	ID	ABO8641	standard; protein; 266 AA.			
	DE	Human secreted/transmembrane protein (PRO) #5.					
	PN	US2003034923-A1.					
PPD	06-MAR-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	24	ID	ABO2693	standard; protein; 266 AA.			
	DE	Human secreted/transmembrane protein (PRO) #5.					
	PN	US2003030062-A1.					
PPD	27-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	25	ID	ABR74847	standard; protein; 266 AA.			
	DE	Human secreted polypeptide PRO180,	SEQ ID NO:10.				
	PN	US2003030056-A1.					
PPD	27-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	26	ID	ABR84609	standard; protein; 266 AA.			
	DE	Human secreted polypeptide PRO180,	SEQ ID NO:10.				
	PN	US2003034926-A1.					
PPD	06-MAR-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	27	ID	ABU84609	standard; protein; 266 AA.			
	DE	Novel human secreted and transmembrane protein PRO180.					
	PN	US2003036140-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	28	ID	ABU85582	standard; protein; 266 AA.			
	DE	Human PRO polypeptide #5.					
	PN	US2003036140-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	29	ID	ABU98742	standard; protein; 266 AA.			
	DE	Novel human secreted and transmembrane protein PRO180.					
	PN	US2003013153-A1.					
PPD	16-JAN-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	30	ID	ABU97957	standard; protein; 266 AA.			
	DE	Novel human secreted and transmembrane protein PRO180.					
	PN	US2003017544-A1.					
PPD	23-JAN-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	31	ID	ABU91663	standard; protein; 266 AA.			
	DE	Novel human secreted and transmembrane protein PRO180.					
	PN	US2003027277-A1.					
PPD	06-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	32	ID	ABU9856	standard; protein; 266 AA.			
	DE	Human PRO polypeptide #5.					
	PN	US2003036141-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	33	ID	ABU86197	standard; protein; 266 AA.			
	DE	Human secreted/transmembrane protein (PRO) #5.					
	PN	US2003036146-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	34	ID	ABU89356	standard; protein; 266 AA.			
	DE	Human secreted/transmembrane protein (PRO) #5.					
	PN	US2003036162-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	35	ID	ABU67410	standard; protein; 266 AA.			
	DE	Human secreted/transmembrane protein (PRO) #5.					
	PN	US2000036162-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	36	ID	ABU84609	standard; protein; 266 AA.			
	DE	Novel human secreted and transmembrane protein PRO180.					
	PN	US2003036137-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	37	ID	ABU84610	standard; protein; 266 AA.			
	DE	Novel human secreted and transmembrane protein PRO180.					
	PN	US2003036137-A1.					
PPD	20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;	
	Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT	38	ID	ABU72450	standard; protein; 266 AA.			
	DE	Novel human secreted and transmembrane protein PRO180.					
	PN	US2003036138-A1.					

PN	US2003003531-A1.	ID	ABU84967 standard; protein; 266 AA.
PD	02-JAN-2003.	DE	Novel human secreted and transmembrane protein PRO180.
PA	(GETH) GENENTECH INC.	DN	US2003032214-A1.
Query Match	Score 1392; DB 6; Length 266;	PN	13-FEB-2003.
Best Local Similarity	Pred. No. 5e-149;	Query Match	Score 1392; DB 6; Length 266;
RESULT 37		Best Local Similarity	100.0%; Pred. No. 5e-149;
ID	ABU90876 standard; protein; 266 AA.	RESULT 47	
DE	Novel human secreted and transmembrane protein PRO180.	ID	A000106 standard; protein; 266 AA.
PN	US2003018173-A1.	DB	Novel human secreted and transmembrane protein PRO180.
PD	23-JAN-2003.	PN	US2003032201-A1.
PA	(GETH) GENENTECH INC.	PD	13-FEB-2003.
Query Match	Score 1392; DB 6; Length 266;	Query Match	Score 1392; DB 6; Length 266;
Best Local Similarity	Pred. No. 5e-149;	Best Local Similarity	100.0%; Pred. No. 5e-149;
RESULT 38		RESULT 48	
ID	ABO33935 standard; protein; 266 AA.	ID	ABO1438 standard; protein; 266 AA.
DE	Human secreted/transmembrane protein PRO180.	DE	Human secreted/transmembrane protein (PRO) #5.
PN	US2003009013-A1.	PN	US2003036124-A1.
PD	09-JAN-2003.	PD	20-FEB-2003.
PA	(GETH) GENENTECH INC.	Query Match	Score 1392; DB 6; Length 266;
Query Match	Score 1392; DB 6; Length 266;	Best Local Similarity	100.0%; Pred. No. 5e-149;
Best Local Similarity	Pred. No. 5e-149;	RESULT 49	
RESULT 39		ID	ABO2083 standard; protein; 266 AA.
ID	ABR99356 standard; protein; 266 AA.	DE	US2003040054-A1.
DB	Human secreted polypeptide PRO180, SEQ ID NO:10.	PN	US20030402102953-A2.
PN	US2003040053-A1.	PD	27-DEC-2002.
PD	27-FEB-2003.	Query Match	Score 1392; DB 6; Length 266;
Query Match	Score 1392; DB 6; Length 266;	Best Local Similarity	100.0%; Pred. No. 5e-149.
Best Local Similarity	Pred. No. 5e-149;	RESULT 50	
RESULT 40		ID	ADA40898 standard; protein; 266 AA.
ID	ABR98746 standard; protein; 266 AA.	DE	Human secreted protein.
DE	Human secreted polypeptide PRO180, SEQ ID NO:10.	PN	(HUMA-) HUMAN GENOME SCI INC.
PN	US2003040064-A1.	PD	Query Match
PD	27-FEB-2003.	Score 1392; DB 6; Length 266;	
Query Match	Score 1392; DB 6; Length 266;	Best Local Similarity	100.0%; Pred. No. 5e-149;
Best Local Similarity	Pred. No. 5e-149;	RESULT 51	
RESULT 41		ID	ABU88657 standard; protein; 266 AA.
ID	ABO16269 standard; protein; 266 AA.	DE	Novel human secreted and transmembrane protein PRO180.
DE	Human secreted polypeptide PRO180, SEQ ID NO:10.	PN	US2003036133-A1.
PN	US200304027267-A1.	PD	20-FEB-2003.
PD	06-FEB-2003.	Query Match	Score 1392; DB 6; Length 266;
Query Match	Score 1392; DB 6; Length 266;	Best Local Similarity	100.0%; Pred. No. 5e-149;
Best Local Similarity	Pred. No. 5e-149;	RESULT 52	
RESULT 42		ID	ABU83352 standard; protein; 266 AA.
ID	ABR92169 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.
DE	Human secreted polypeptide PRO180, SEQ ID NO:10.	PN	US2003036160-A1.
PN	US2003036160-A1.	PD	20-FEB-2003.
PD	20-FEB-2003.	Query Match	Score 1392; DB 6; Length 266;
Query Match	Score 1392; DB 6; Length 266;	Best Local Similarity	100.0%; Pred. No. 5e-149;
Best Local Similarity	Pred. No. 5e-149;	RESULT 53	
RESULT 43		ID	ABO18810 standard; protein; 266 AA.
ID	ABR78231 standard; protein; 266 AA.	DE	Novel human secreted and transmembrane protein PRO180.
DE	Human secreted/transmembrane protein (PRO) #5.	PN	US2003022294-A1.
PN	US2003044925-A1.	PD	30-JAN-2003.
PD	06-MAR-2003.	Query Match	Score 1392; DB 6; Length 266;
Query Match	Score 1392; DB 6; Length 266;	Best Local Similarity	100.0%; Pred. No. 5e-149;
Best Local Similarity	Pred. No. 5e-149;	RESULT 54	
RESULT 44		ID	ABO188153 standard; protein; 266 AA.
ID	ABR78231 standard; protein; 266 AA.	DE	Human secreted and transmembrane protein PRO180, SEQ ID NO:10.
DE	Human secreted polypeptide PRO180, SEQ ID NO:10.	PN	US2003022725-A1.
PN	US2003054474-A1.	PD	06-FEB-2003.
PD	20-MAR-2003.	Query Match	Score 1392; DB 6; Length 266;
Query Match	Score 1392; DB 6; Length 266;	Best Local Similarity	100.0%; Pred. No. 5e-149.
Best Local Similarity	Pred. No. 5e-149;	RESULT 55	
RESULT 45		ID	ABR59189 standard; protein; 266 AA.
ID	ABU1952 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.
DE	Novel human secreted and transmembrane protein PRO180.	PN	US2003027244-A1.
PN	US2003018183-A1.	PD	06-FEB-2003.
PD	23-JAN-2003.	Query Match	Score 1392; DB 6; Length 266;
Query Match	Score 1392; DB 6; Length 266;	Best Local Similarity	100.0%; Pred. No. 5e-149;
Best Local Similarity	Pred. No. 5e-149;	RESULT 56	
RESULT 46		ID	ABO19115 standard; protein; 266 AA.
ID	ABO19115 standard; protein; 266 AA.	DE	Novel human secreted and transmembrane protein PRO180.

PN US2003036118-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABO1133 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003036123-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABR66751 standard; polypeptide PRO180, SEQ ID NO:10.
 DE Human secreted polypeptide PRO180 , SEQ ID NO:10.
 PN US2003036148-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABO15964 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003040060-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABO13670 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US20030404916-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABO171506 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180.
 PN US200303855-A1.
 PD 16-JAN-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABU65573 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein, SEQ ID 10.
 PN US2003036156-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABO07421 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003032117-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID AB003608 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003036128-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABP67056 standard; Protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003032126-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABO13980 standard; protein; 266 AA.
 DE Novel human secreted protein #9.
 PN US2003028003-A1.

PD 06-FEB-2003.
 PA (ROSE /) ROSEN C A.
 PA (FENG /) FENG P.
 PA (RUBE /) RUBEN S M.
 PA (EBNE /) EBNER R.
 PA (OLSE /) OLSEN H S.
 PA (NIJU /) NI J.
 PA (WEIY /) WEI Y.
 PA (SOPP /) SOPPET D R.
 PA (MOOR /) MOORE P A.
 PA (KYAW /) KYAW H.
 PA (LAFL /) LAFLEUR D W.
 PA (SHIV /) SHIV Y.
 PA (JANA /) JANAT F.
 PA (ENDR /) ENDRESS G A.
 PA (CART /) CARTER K C.
 PA (BIRSE /) BIRSE C E.
 Query Match 100.0%; Score 1392; DB 6; Pred. No. 5e-149; ID ABO15659 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003054483-A1.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Pred. No. 5e-149; ID ABU55840 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein, PRO180.
 PN US2003022298-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Pred. No. 5e-149; ID ABU72287 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2002182638-A1.
 PD 05-DEC-2002.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Pred. No. 5e-149; ID ABU5268 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003032102-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Pred. No. 5e-149; ID ABU05213 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003036117-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Pred. No. 5e-149; ID ABU71116 standard; protein; 266 AA.
 DE Human PRO180 protein.
 PN US2003036143-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Pred. No. 5e-149; ID ABU07726 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003033210-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Pred. No. 5e-149; ID ABU07726 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003033210-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Pred. No. 5e-149; ID ABR69967 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.

RESULT 66
 ID ABO13980 standard; protein; 266 AA.
 DE Novel human secreted protein #9.
 PN US2003028003-A1.

PN US2003032138-A1.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 75
 ID ABR69300 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003036132-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 76
 ID ABO01441 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US200308353-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 77
 ID ABU81243 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003017542-A1.
 PD 23-JAN-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 78
 ID ABR60040 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003032137-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 79
 ID ABU90900 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003018168-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 80
 ID ABR67775 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003027265-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 81
 ID ABR65163 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003027268-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 82
 ID ABR68385 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US20030321774-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 83
 ID ABR71797 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003032135-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 84
 ID ABU59199 standard; protein; 266 AA.
 DE Human secreted/transmembrane polypeptide PRO180.

DB Human secreted/transmembrane protein, #9.
 PN US2003027162-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 85
 ID ABU85377 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003022295-A1.
 PD 30-JAN-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 86
 ID ABU88067 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003022297-A1.
 PD 30-JAN-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 87
 ID ABU83047 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003032105-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 88
 ID ABU91903 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003032123-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 89
 ID ABU90451 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003032108-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 90
 ID ABU83952 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003032111-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 91
 ID ABU93613 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003032119-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 92
 ID ABO25896 standard; protein; 266 AA.
 DE Human PRO180 polypeptide.
 PN US2002127576-A1.
 PD 12-FEB-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 93
 ID ABR64858 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003027263-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 94
 ID ABO27281 standard; protein; 266 AA.
 DE Human secreted/transmembrane polypeptide PRO180.

PN	US2003009012-A1.	PA (GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
PD	09-JAN-2003.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PA	(GETH) GENENTECH INC.	RESULT 105	ID ABU81742 standard; protein; 266 AA.				
	Query Match		DE Novel human secreted and transmembrane protein PRO180.				
	Best Local Similarity		PN US2003032104-A1.				
RESULT 95	ID ABR68690 standard; protein; 266 AA.	PD 13-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
	DE Human secreted polypeptide PRO180, SEQ ID NO:10.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US20030327271-A1.		RESULT 106	ID ABU65906 standard; protein; 266 AA.			
PD	05-FEB-2003.		DE Novel human secreted and transmembrane protein PRO180.				
Query Match	100.0%;	Score 1392;	DB 6;	Length 266;			
Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT 96	ID ABR65056 standard; protein; 266 AA.	PD 20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
	DE Human secreted/transmembrane protein (PRO) #5.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003036125-A1.		RESULT 107	ID ABU81146 standard; protein; 266 AA.			
PD	20-FEB-2003.		DE Human secreted polypeptide PRO180.				
Query Match	100.0%;	Score 1392;	DB 6;	Length 266;			
Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT 97	ID ABR99051 standard; protein; 266 AA.	PD 20-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
	DE Human secreted polypeptide PRO180, SEQ ID NO:10.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003040068-A1.		RESULT 108	ID ABR59735 standard; protein; 266 AA.			
PD	06-FEB-2003.		DE Human secreted polypeptide PRO180, SEQ ID NO:10.				
Query Match	100.0%;	Score 1392;	DB 6;	Length 266;			
Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT 98	ID ABR56935 standard; protein; 266 AA.	PD 06-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
	DE Human secreted polypeptide #5.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003027280-A1.		RESULT 109	ID ABU9323 standard; protein; 266 AA.			
PD	06-FEB-2003.		DE Novel human secreted and transmembrane protein PRO180.				
Query Match	100.0%;	Score 1392;	DB 6;	Length 266;			
Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT 99	ID ABU85887 standard; protein; 266 AA.	PD 06-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
	DE Novel human secreted and transmembrane protein PRO180.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003022300-A1.		RESULT 110	ID ABU9976 standard; protein; 266 AA.			
PD	06-FEB-2003.		DE Novel human secreted and transmembrane protein PRO180.				
Query Match	100.0%;	Score 1392;	DB 6;	Length 266;			
Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT 100	ID ABR82174 standard; protein; 266 AA.	PD 06-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
	DE Novel human secreted and transmembrane protein PRO180.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US20030316136-A1.		RESULT 111	ID ABR6446 standard; protein; 266 AA.			
PD	06-FEB-2003.		DE Novel human secreted polypeptide PRO180, SEQ ID NO:10.				
Query Match	100.0%;	Score 1392;	DB 6;	Length 266;			
Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT 101	ID ABR87185 standard; protein; 266 AA.	PD 06-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
	DE Human secreted polypeptide #5.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US20030316138-A1.		RESULT 112	ID ABR90364 standard; protein; 266 AA.			
PD	06-FEB-2003.		DE Human secreted polypeptide PRO180, SEQ ID NO:10.				
Query Match	100.0%;	Score 1392;	DB 6;	Length 266;			
Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT 102	ID ABR83657 standard; protein; 266 AA.	PD 06-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
	DE Human secreted/transmembrane protein (PRO) #5.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003032109-A1.		RESULT 113	ID ABO53261 standard; protein; 266 AA.			
PD	13-FEB-2003.		DE Novel human secreted and transmembrane protein PRO180.				
Query Match	100.0%;	Score 1392;	DB 6;	Length 266;			
Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT 103	ID ABO08031 standard; protein; 266 AA.	PD 13-FEB-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
	DE Human PRO polypeptide #5.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003030066-A1.		RESULT 114	ID ABU58905 standard; protein; 266 AA.			
PD	27-FEB-2003.		DE Human secreted/transmembrane protein, #9.				
Query Match	100.0%;	Score 1392;	DB 6;	Length 266;			
Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT 104	ID ABU92476 standard; protein; 266 AA.	PD 06-MAR-2003.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;
	DE Human secreted/transmembrane protein PRO180.		Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US20030305684-A1.		RESULT 115	ID ABU58905 standard; protein; 266 AA.			
PD	06-MAR-2003.		DE Human secreted/transmembrane protein US2002142961-A1.				

ID	ABU98263	standard; protein; 266 AA.	ID	ABO09861	standard; protein; 266 AA.
DE	Novel human secreted and transmembrane protein PRO180.	DE	Human secreted/transmembrane protein (PRO) #5.		
PN	US2003183493-A1.	PN	US2003017543-A1.		
PD	05-DEC-2002.	PD	23-JAN-2003.		
PA	(GETH) GENENTECH INC.	Query Match	100.0%; Score 1392; DB 6;		
	Best Local Similarity 100.0%; Pred. No. 5e-149;	Best Local Similarity 100.0%; Pred. No. 5e-149;	Length 266;		
RESULT 136	ID ABU87490 standard; protein; 266 AA.	RESULT 146	ID ABO08946 standard; protein; 266 AA.		
DE	Human PRO polypeptide #5.	DE	Human secreted/transmembrane protein (PRO) #5.		
PN	US2003022293-A1.	PN	US2003036152-A1.		
PD	20-JAN-2003.	PD	20-FEB-2003.		
PA	Query Match 100.0%; Score 1392; DB 6;	Query Match 100.0%; Score 1392; DB 6;	Length 266;		
	Best Local Similarity 100.0%; Pred. No. 5e-149;	Best Local Similarity 100.0%; Pred. No. 5e-149;	Length 266;		
RESULT 137	ID ABU91358 standard; protein; 266 AA.	RESULT 147	ID ABU956439 standard; protein; 266 AA.		
DE	Human PRO polypeptide #5.	DE	Human PRO polypeptide #1.		
PN	US2003032128-A1.	PN	US2003027933-A1.		
PD	13-FEB-2003.	PD	06-FEB-2003.		
PA	Query Match 100.0%; Score 1392; DB 6;	Query Match 100.0%; Score 1392; DB 6;	Length 266;		
	Best Local Similarity 100.0%; Pred. No. 5e-149;	Best Local Similarity 100.0%; Pred. No. 5e-149;	Length 266;		
RESULT 138	ID ABU89268 standard; protein; 266 AA.	RESULT 148	ID ABU10820 standard; protein; 266 AA.		
DE	Novel human secreted and transmembrane protein PRO180.	DE	Human PRO polypeptide #6.		
PN	US2003036634-A1.	PN	US2002123463-A1.		
PD	20-FEB-2003.	PD	05-SEP-2002.		
PA	(GETH) GENENTECH INC.	PA	(GETH) GENENTECH INC.		
	Query Match 100.0%; Score 1392; DB 6;	Query Match 100.0%; Score 1392; DB 6;	Length 266;		
RESULT 139	Best Local Similarity 100.0%; Pred. No. 5e-149;	Best Local Similarity 100.0%; Pred. No. 5e-149;	Length 266;		
ID	ABD84572 standard; protein; 266 AA.	RESULT 149	ID ABU10514 standard; protein; 266 AA.		
DE	Human secreted/transmembrane protein (PRO) #5.	DE	Human secreted/transmembrane protein #5.		
PN	US2003032116-A1.	PN	US2002127584-A1.		
PD	13-FEB-2003.	PD	12-SEP-2002.		
PA	Query Match 100.0%; Score 1392; DB 6;	PA	(GETH) GENENTECH INC.		
	Best Local Similarity 100.0%; Pred. No. 5e-149;	Query Match 100.0%; Score 1392; DB 6;	Length 266;		
RESULT 140	ID ABR9662 standard; protein; 266 AA.	Best Local Similarity 100.0%; Pred. No. 5e-149;	Length 266;		
DE	Human secreted polypeptide PRO180, SEQ ID NO:10.	RESULT 150	ID ABU81572 standard; protein; 266 AA.		
PN	US2003031122-A1.	DE	Novel human secreted and transmembrane protein PRO180.		
PD	13-FEB-2003.	PN	US2002171164-A1.		
PA	Query Match 100.0%; Score 1392; DB 6;	PA	(GETH) GENENTECH INC.		
	Best Local Similarity 100.0%; Pred. No. 5e-149;	Query Match 100.0%; Score 1392; DB 6;	Length 266;		
RESULT 141	ID ABR9662 standard; protein; 266 AA.	Best Local Similarity 100.0%; Pred. No. 5e-149;	Length 266;		
DE	Human secreted polypeptide PRO180, SEQ ID NO:10.	RESULT 151	ID ABU81572 standard; protein; 266 AA.		
PN	US2003031122-A1.	DE	Novel human secreted and transmembrane protein PRO180.		
PD	20-FEB-2003.	PN	US2002171164-A1.		
PA	Query Match 100.0%; Score 1392; DB 6;	PA	(GETH) GENENTECH INC.		
	Best Local Similarity 100.0%; Pred. No. 5e-149;	Query Match 100.0%; Score 1392; DB 6;	Length 266;		
RESULT 142	ID ABU0039 standard; protein; 266 AA.	Best Local Similarity 100.0%; Pred. No. 5e-149;	Length 266;		
DE	Human PRO protein #5.	RESULT 152	ID ABU95523 standard; protein; 266 AA.		
PN	US2003036139-A1.	DE	Novel human secreted and transmembrane protein PRO180.		
PD	05-DEC-2002.	PN	US2003023042-A1.		
PA	(GETH) GENENTECH INC.	PA	(GETH) GENENTECH INC.		
	Query Match 100.0%; Score 1392; DB 6;	Query Match 100.0%; Score 1392; DB 6;	Length 266;		
RESULT 143	Best Local Similarity 100.0%; Pred. No. 5e-149;	Best Local Similarity 100.0%; Pred. No. 5e-149;	Length 266;		
ID	ABU2114 standard; protein; 266 AA.	RESULT 153	ID ABU96732 standard; protein; 266 AA.		
DE	Novel human secreted and transmembrane protein PRO180.	DE	Novel human secreted and transmembrane protein PRO180.		
PN	US2002183494-A1.	PN	US20032140-A1.		
PD	23-JAN-2003.	PD	13-FEB-2003.		
PA	Query Match 100.0%; Score 1392; DB 6;	Query Match 100.0%; Score 1392; DB 6;	Length 266;		
	Best Local Similarity 100.0%; Pred. No. 5e-149;	Best Local Similarity 100.0%; Pred. No. 5e-149;	Length 266;		
RESULT 144	ID ABU3308 standard; protein; 266 AA.	RESULT 154	ID ABR70577 standard; protein; 266 AA.		
DE	Human PRO polypeptide #5.	DE	Human secreted polypeptide PRO180, SEQ ID NO:10.		
PN	US2003017541-A1.	PN	US2003040076-A1.		
PD	23-JAN-2003.	PD	27-FEB-2003.		
PA	Query Match 100.0%; Score 1392; DB 6;	PA	(GETH) GENENTECH INC.		
	Best Local Similarity 100.0%; Pred. No. 5e-149;	Query Match 100.0%; Score 1392; DB 6;	Length 266;		
RESULT 145	ID ABU3308 standard; protein; 266 AA.	Best Local Similarity 100.0%; Pred. No. 5e-149;	Length 266;		
DE	Human PRO polypeptide #5.	RESULT 155	ID ABR70577 standard; protein; 266 AA.		
PN	US2003017541-A1.	DE	Human secreted polypeptide PRO180, SEQ ID NO:10.		
PD	23-JAN-2003.	PN	US2003040076-A1.		
PA	Query Match 100.0%; Score 1392; DB 6;	PA	(GETH) GENENTECH INC.		
	Best Local Similarity 100.0%; Pred. No. 5e-149;	Query Match 100.0%; Score 1392; DB 6;	Length 266;		

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 155
 ID ABO04928 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003008352-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 156
 ID ABO08336 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US200304922-A1.
 PD 06-MAR-2003.

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 157
 ID ABO8511 standard; protein; 266 AA.
 DE Human secreted and transmembrane polypeptide PRO180.
 PN US2002197615-A1.
 PD 26-DEC-2002.

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 158
 ID AB034025 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003017981-A1.
 PD 23-JAN-2003.

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 159
 ID ABO05543 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003032118-A1.
 PD 13-FEB-2003.

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 160
 ID ABR73932 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003036135-A1.
 PD 20-FEB-2003.

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 161
 ID ABR9524 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054455-A1.
 PD 20-MAR-2003.

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 162
 ID ABR80821 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003049741-A1.
 PD 13-MAR-2003.

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 163
 ID ABR81126 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003049743-A1.
 PD 13-MAR-2003.

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 164
 ID ABM00822 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003049769-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 165
 ID ABR88424 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068743-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 166
 ID ABM77245 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003044479-A1.
 PD 20-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 167
 ID ABO28729 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068605-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 168
 ID ABO31474 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068725-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 169
 ID ABM07891 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068752-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 170
 ID ABO40371 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068632-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 171
 ID ABO35796 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003068701-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 172
 ID ABO43935 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003068755-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 173
 ID ADA77762 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003073180-A1.

PD 17-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID NO:10.

RESULT 174
 ID ABM2730 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104539-A1.
 PD 05-JUN-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID NO:10.

RESULT 175
 ID AB02998 standard; protein: 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003036131-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID NO:10.

RESULT 176
 ID ABR0254 standard; protein: 266 AA. APR-2003.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003030075-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID NO:10.

RESULT 177
 ID ABM17168 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US20030354459-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID NO:10.

RESULT 178
 ID AB094914 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200303044930-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID NO:10.

RESULT 179
 ID ABR05219 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200303040071-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID NO:10.

RESULT 180
 ID ADB17059 standard; protein: 266 AA.
 DE Human transmembrane PRO polypeptide (SEQID 2).
 PN US2003050462-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID NO:10.

RESULT 181
 ID ABO21457 standard; protein: 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US20030504471-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID NO:10.

RESULT 182
 ID ABR97721 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US20030504452-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; ID NO:10.

RESULT 183
 ID ABR24540 standard; protein: 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.

PN US2003065159-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 193 ID ADA37534 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003008297-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 194 ID ABM1551 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200306447-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 195 ID ABM6552 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003073184-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 196 ID ABM15948 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003064463-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 197 ID AB027509 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003064451-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 198 ID ABM29000 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068721-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 199 ID ABM06976 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068699-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 200 ID ABM1070 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068707-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 201 ID ABM09416 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003073175-A1.

PD 17-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 202 ID ABO1286 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068695-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 203 ID ABO36101 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003068703-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 204 ID ABO43320 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003068732-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 205 ID ABM76320 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003082717-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 206 ID ABM76026 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104548-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 207 ID ABM25645 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104542-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 208 ID ABM25930 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104543-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 209 ID ADA21220 standard; protein; 266 AA.
 DE Human secreted/transmembrane polypeptide PRO180.
 PN US2003104540-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 210 ID ABO03303 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003036127-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 211 ID ABO02388 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.

DE Human secreted/transmembrane protein (PRO) #5.
 PN US003040061-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 21
 ID ABR44239 standard; protein; 266 AA.
 DE Human secreted/transmembrane polypeptide PRO 180.
 PN US0030408172-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 213
 ID ABR90559 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180; SEQ ID NO:10.
 PN US2003016130-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 214
 ID ABR73627 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180; SEQ ID NO:10.
 PN US2003054468-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 215
 ID ABR016879 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003054470-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 216
 ID ABR44304 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180; SEQ ID NO:10.
 PN US2003044917-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 217
 ID ABR15811 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180; SEQ ID NO:10.
 PN US2003044929-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 218
 ID ABR71187 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180; SEQ ID NO:10.
 PN US200305980-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 219
 ID ABR93084 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180; SEQ ID NO:10.
 PN US2003056465-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 220
 ID ABR31389 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180; SEQ ID NO:10.
 PN US2003054478-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 221
 ID ADD10007 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein; PRO180.
 PN US2003059831-A1.
 PD 27-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 222
 ID ABR87814 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180; SEQ ID NO:10.
 PN US2003068718-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 223
 ID ABO227814 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003064454-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 224
 ID ABO29949 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003064461-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 225
 ID ABO233158 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003068724-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 226
 ID ABM04846 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180; SEQ ID NO:10.
 PN US2003068727-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 227
 ID ABM04846 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180; SEQ ID NO:10.
 PN US2003068772-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 228
 ID ABC36406 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068714-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 229
 ID ABC35491 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003068758-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 230

ID ABO39456 standard; protein, 266 AA.	Score 1392; DB 6;	Length 266;	PD 20-MAR-2003.
DE Human secreted/transmembrane protein (PRO) #5.			PA (GETH) GENENTECH INC.
PN US2003068775-A1.			Query Match 100.0%; Pred. No. 5e-149;
PD 10-APR-2003			Best Local Similarity 100.0%;
PA (GETH) GENENTECH INC.			Score 1392; DB 6;
Query Match 100.0%;	Score 1392; DB 6;	Length 266;	PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%;	Pred. No. 5e-149;		Query Match 100.0%;
RESULT 231			Score 1392; DB 6;
ID ABO10311 standard; protein, 266 AA.	Score 1392; DB 6;	Length 266;	PA (GETH) GENENTECH INC.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.			Query Match 100.0%;
PN US2003069407-A1.			Score 1392; DB 6;
PD 10-APR-2003.			PA (GETH) GENENTECH INC.
PA (GETH) GENENTECH INC.			Query Match 100.0%;
Query Match 100.0%;	Score 1392; DB 6;	Length 266;	Score 1392; DB 6;
Best Local Similarity 100.0%;	Pred. No. 5e-149;		Best Local Similarity 100.0%;
RESULT 232			Score 1392; DB 6;
ID ABO11816 standard; protein, 266 AA.	Score 1392; DB 6;	Length 266;	PA (GETH) GENENTECH INC.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.			Query Match 100.0%;
PN US2003104555-A1.			Score 1392; DB 6;
PD 05-JUN-2003.			PA (GETH) GENENTECH INC.
PA (GETH) GENENTECH INC.			Query Match 100.0%;
Query Match 100.0%;	Score 1392; DB 6;	Length 266;	Score 1392; DB 6;
Best Local Similarity 100.0%;	Pred. No. 5e-149;		Best Local Similarity 100.0%;
RESULT 233			Score 1392; DB 6;
ID ABO52002 standard; protein, 266 AA.	Score 1392; DB 6;	Length 266;	PA (GETH) GENENTECH INC.
DE Human PRO polypeptide #5.			Query Match 100.0%;
PN US2003149761-A1.			Score 1392; DB 6;
PD 13-MAR-2003.			Length 266;
PA (GETH) GENENTECH INC.			PA (GETH) GENENTECH INC.
Query Match 100.0%;	Score 1392; DB 6;	Length 266;	Query Match 100.0%;
Best Local Similarity 100.0%;	Pred. No. 5e-149;		Score 1392; DB 6;
RESULT 234			Length 266;
ID ABO52307 standard; protein, 266 AA.	Score 1392; DB 6;	Length 266;	PA (GETH) GENENTECH INC.
DE Human PRO polypeptide #5.			Query Match 100.0%;
PN US2003149771-A1.			Score 1392; DB 6;
PD 13-MAR-2003.			Length 266;
PA (GETH) GENENTECH INC.			PA (GETH) GENENTECH INC.
Query Match 100.0%;	Score 1392; DB 6;	Length 266;	Query Match 100.0%;
Best Local Similarity 100.0%;	Pred. No. 5e-149;		Score 1392; DB 6;
RESULT 235			Length 266;
ID ADA19864 standard; protein, 266 AA.	Score 1392; DB 6;	Length 266;	PA (GETH) GENENTECH INC.
DE Novel human secreted and transmembrane protein PRO180.			Query Match 100.0%;
PN US2003069394-A1.			Score 1392; DB 6;
PD 10-APR-2003.			Length 266;
PA (GETH) GENENTECH INC.			PA (GETH) GENENTECH INC.
Query Match 100.0%;	Score 1392; DB 6;	Length 266;	Query Match 100.0%;
Best Local Similarity 100.0%;	Pred. No. 5e-149;		Score 1392; DB 6;
RESULT 236			Length 266;
ID ABO23625 standard; protein, 266 AA.	Score 1392; DB 6;	Length 266;	PA (GETH) GENENTECH INC.
DE Human secreted/transmembrane protein (PRO) #5.			Query Match 100.0%;
PN US2003312134-A1.			Score 1392; DB 6;
PD 13-FEB-2003.			Length 266;
PA (GETH) GENENTECH INC.			PA (GETH) GENENTECH INC.
Query Match 100.0%;	Score 1392; DB 6;	Length 266;	Query Match 100.0%;
Best Local Similarity 100.0%;	Pred. No. 5e-149;		Score 1392; DB 6;
RESULT 237			Length 266;
ID ADB17247 standard; protein, 266 AA.	Score 1392; DB 6;	Length 266;	PA (GETH) GENENTECH INC.
DE Human transmembrane PRO polypeptide (SeqID 2).			Query Match 100.0%;
PN US2003050465-A1.			Score 1392; DB 6;
PD 13-MAR-2003.			Length 266;
PA (GETH) GENENTECH INC.			PA (GETH) GENENTECH INC.
Query Match 100.0%;	Score 1392; DB 6;	Length 266;	Query Match 100.0%;
Best Local Similarity 100.0%;	Pred. No. 5e-149;		Score 1392; DB 6;
RESULT 238			Length 266;
ID ADA17551 standard; protein, 266 AA.	Score 1392; DB 6;	Length 266;	PA (GETH) GENENTECH INC.
DE Human PRO180 polypeptide.			Query Match 100.0%;
PN US2003054987-A1.			Score 1392; DB 6;
PD 20-MAR-2003.			Length 266;
PA (GETH) GENENTECH INC.			PA (GETH) GENENTECH INC.
Query Match 100.0%;	Score 1392; DB 6;	Length 266;	Query Match 100.0%;
Best Local Similarity 100.0%;	Pred. No. 5e-149;		Score 1392; DB 6;
RESULT 239			Length 266;
ID ABR97111 standard; protein, 266 AA.	Score 1392; DB 6;	Length 266;	PA (GETH) GENENTECH INC.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.			Query Match 100.0%;
PN US2003054481-A1.			Score 1392; DB 6;
PD 10-APR-2003.			Length 266;

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted/transmembrane protein PRO180.
RESULT 249
 ID ABO040676 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US20030368684-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 250
 ID ABM35323 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180-A1.
 PN US2003073179-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 251
 ID ABM33036 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200308374-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 252
 ID AB053612 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US20030409773-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted/transmembrane protein (PRO) #5.
RESULT 253
 ID ABO01172 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US20030409777-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted/transmembrane protein (PRO) #5.
RESULT 254
 ID ABU09166 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US20030400555-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted/transmembrane protein (PRO) #5.
RESULT 255
 ID AB004218 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003036164-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted/transmembrane protein (PRO) #5.
RESULT 256
 ID ABO05848 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003040074-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted/transmembrane protein (PRO) #5.
RESULT 257
 ID ABM18388 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054480-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 258
 ID ADA27659 standard; protein; 266 AA.

PA (GETH) GENENTECH INC. Query Match 100 %; Score 1392; DB 6; Length 266;
 Best Local Similarity 100 %; Pred. No. 5e-149;
 RESULT 268 ID ABO3541 standard; protein; 266 AA. DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068773-A1.
 PA (GETH) GENENTECH INC. Query Match 100 %; Score 1392; DB 6; Length 266;
 Best Local Similarity 100 %; Pred. No. 5e-149;
 RESULT 269 ID ABM32781 standard; protein; 266 AA. DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003073185-A1.
 PA (GETH) GENENTECH INC. Query Match 100 %; Score 1392; DB 6; Length 266;
 Best Local Similarity 100 %; Pred. No. 5e-149;
 RESULT 270 ID ABM22595 standard; protein; 266 AA. DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003087373-A1.
 PA (GETH) GENENTECH INC. Query Match 100 %; Score 1392; DB 6; Length 266;
 Best Local Similarity 100 %; Pred. No. 5e-149;
 RESULT 271 ID ABM74806 standard; protein; 266 AA. DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003096553-A1.
 PA (GETH) GENENTECH INC. Query Match 100 %; Score 1392; DB 6; Length 266;
 Best Local Similarity 100 %; Pred. No. 5e-149;
 RESULT 272 ID ADA70554 standard; protein; 266 AA. DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003073173-A1.
 PA (GETH) GENENTECH INC. Query Match 100 %; Score 1392; DB 6; Length 266;
 Best Local Similarity 100 %; Pred. No. 5e-149;
 RESULT 273 ID ABR9196 standard; protein; 266 AA. DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054458-A1.
 PA (GETH) GENENTECH INC. Query Match 100 %; Score 1392; DB 6; Length 266;
 Best Local Similarity 100 %; Pred. No. 5e-149;
 RESULT 274 ID ABM03347 standard; protein; 266 AA. DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003059886-A1.
 PA (GETH) GENENTECH INC. Query Match 100 %; Score 1392; DB 6; Length 266;
 Best Local Similarity 100 %; Pred. No. 5e-149;
 RESULT 275 ID ABR88289 standard; protein; 266 AA. DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003049758-A1.
 PA (GETH) GENENTECH INC. Query Match 100 %; Score 1392; DB 6; Length 266;
 Best Local Similarity 100 %; Pred. No. 5e-149;
 RESULT 276 ID ABR88594 standard; protein; 266 AA. DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003049772-A1.
 PA (GETH) GENENTECH INC. Query Match 100 %; Score 1392; DB 6; Length 266;
 Best Local Similarity 100 %; Pred. No. 5e-149;
 RESULT 277 ID ABM16558 standard; protein; 266 AA. DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003088737-A1.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Result 287

ID ABM75721 standard; protein; 266 AA. SEQ ID NO:10.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104547-A1.
 PD 05-JUN-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Result 288

ID ABM34001 standard; protein; 266 AA. SEQ ID NO:10.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003096359-A1.
 PD 22-MAY-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Result 289

ID ABM34306 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003100061-A1.
 PD 29-MAY-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Result 290

ID AB020237 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003032125-A1.
 PD 13-FEB-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Result 291

ID AB021152 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003054454-A1.
 PD 20-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Result 292

ID AB022067 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003054477-A1.
 PD 20-MAR-2003.

PA (GETH) GENENTECH INC. AD20036 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003055222-A1.
 PD 20-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Result 293

ID ABO14167 standard; protein; 266 AA.
 DE Human secreted/transmembrane polypeptide PRO 180.
 PN US2003050601-A1.
 PD 27-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Result 294

ID ABO14167 standard; protein; 266 AA.
 DE Human secreted/transmembrane polypeptide PRO 180.
 PN US2003054460-A1.
 PD 27-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Result 295

ID ABR66501 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054460-A1.
 PD 20-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Result 296

RESULT 296
 ID ADA91239 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003059832-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 ID ABR85679 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003049753-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 297
 ID ABR99661 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003049753-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 298
 ID ABR99661 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003049753-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 299
 ID ABM00212 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003073172-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 300
 ID ABM00517 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003073172-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 301
 ID ABO29644 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068700-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 302
 ID ABM23510 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068736-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 303
 ID ABM29305 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068679-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6;
 Best Local Similarity 100.0%; Pred. No. 5e-149;

PD 17-APR-2003.
PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABR9644 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RN 306 ID ABR20460 standard; protein; 266 AA. SEQ ID NO:10.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABR1281 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
RN 307 ID ADR803092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABR16574 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
RN 308 ID ABO18200 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABO22627 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
RN 309 ID ABO22932 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032765-A1.
PD 05-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABR92474 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RN 310 ID ABR81431 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABR031064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABR81431 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RN 311 ID ABR81431 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049744-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABR037016 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
RN 312 ID ABR037016 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABR037016 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
RN 313 ID ABR037016 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABR037016 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
RN 314 ID ABR77855 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; ID ABO35186 standard; protein; 266 AA.
DE Human PRO polypeptide #5.

PN US2003068738-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 325
 ID ABM2035 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200304540-A1.
 PD 05-JUN-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 326
 ID AB047427 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003049742-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 327
 ID AB047732 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003049747-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 328
 ID AB048342 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003049750-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 329
 ID AB051392 standard; protein; 266 AA.
 DE Human pro polypeptide #5.
 PN US2003049766-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 330
 ID AB051697 standard; protein; 266 AA.
 DE Human pro polypeptide #5.
 PN US2003049767-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 331
 ID AB050477 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003049779-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 332
 ID ABR19601 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003040059-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 333
 ID ABM16863 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003040078-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 334
 ID ABO17895 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003044918-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 335
 ID ABO20847 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003032132-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 336
 ID ABR96806 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054462-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 337
 ID ADA38464 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003059780-A1.
 PD 27-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 338
 ID ABM12161 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003064415-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 339
 ID ABM16253 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003064449-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 340
 ID ABM24120 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003064441-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 341
 ID ABM14601 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068696-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 342
 ID ABM04432 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US20030686712-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 343
 ID ABM06671 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200306712-A1.

PN US2003068730-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 344
 ID ABM09111 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003073174-A1.
 PD 17-APR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 345
 ID ABO39151 standard; protein; 266 AA.
 DB Human secreted/transmembrane protein (PRO) #5.
 PN US2003068775-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 346
 ID ABM75416 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104545-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 347
 ID ABM25340 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104541-A1.
 PD 05-JUN-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 348
 ID ABM19850 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104554-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 349
 ID ABO46756 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003049762-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 350
 ID ABO47061 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003049765-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 351
 ID ABO83079 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003049752-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 352
 ID ABR1492 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003021333-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 353
 ID ABR72102 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003032136-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 354
 ID ABR98441 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003036129-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 355
 ID ABO6811 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003040053-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 356
 ID ABR84764 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003040057-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 357
 ID ABR73122 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054467-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 358
 ID ABR76416 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003044932-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 359
 ID ABR73017 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003027270-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 360
 ID ABM18083 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054459-PN.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 361
 ID ABO20542 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003032126-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 362
 ID ABO25285 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003054463-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 6; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 363
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 ID ABM0590 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003054456-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 364
 ID ABR93999 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003059879-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 365
 ID Ad92585 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003050407-A1.
 PD 27-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 366
 ID AB79906 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003049738-A1.
 PD 13-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 367
 ID ABM1246 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200304469-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 368
 ID ABO2853 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003064453-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 369
 ID ABO10559 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003064466-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 370
 ID ABO30864 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003064468-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 371
 ID ABM27170 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003060760-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 372
 ID ABM29915 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068769-A1.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 373
 ID ABM05451 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003045700-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 374
 ID ABM15516 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068658-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 375
 ID ABM08501 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068759-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 376
 ID ABO4201 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003049748-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 377
 ID ABO37931 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068765-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 378
 ID ABO45841 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003049754-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 379
 ID ABM66644 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068686-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 380
 ID ADB20122 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003082767-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 381
 ID ABM19545 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104552-A1.

PD	05-JUN-2003.	PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;
	(GETH) GENENTECH INC.			Best Local Similarity	100.0%;	Pred. No. 5e-149;		
	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;			
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	383	ID	AB049257 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.			
	US20030349774-A1.	PN						
	PD	13-MAR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	383	ID	AB049562 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.			
	US20030349775-A1.	PN						
	PD	13-MAR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	384	ID	ADA78374 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.			
	US2003073181-A1.	PN						
	PD	17-APR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	385	ID	ABR88119 standard; protein; 266 AA.	DE	Human secreted polypeptide PRO180, SEQ ID NO:10.			
	US200306720-A1.	PN						
	PD	10-APR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	386	ID	ADU0313 standard; protein; 266 AA.	DE	Human secreted/transmembrane polypeptide PRO 180.			
	US2003027992-A1.	PN						
	PD	06-FEB-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	387	ID	ABM26865 standard; protein; 266 AA.	DE	Human secreted polypeptide PRO180, SEQ ID NO:10.			
	US2003068739-A1.	PN						
	PD	10-APR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	388	ID	ABR03262 standard; protein; 266 AA.	DE	Human secreted polypeptide PRO180, SEQ ID NO:10.			
	US2003068763-A1.	PN						
	PD	10-APR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 6;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	389	ID	ABO39761 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.			
	US2003068689-A1.	PN						
	PD	10-APR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	390	ID	ABO49867 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.			
	US20030349776-A1.	PN						
	PD	13-MAR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	391	ID	ABO50782 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.			
	US2003049780-A1.	PN						
	PD	13-MAR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	392	ID	ABO5238 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.			
	US2003036126-A1.	PN						
	PD	20-FEB-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	393	ID	ABR74542 standard; protein; 266 AA.	DE	Human secreted polypeptide PRO180, SEQ ID NO:10.			
	US2003044924-A1.	PN						
	PD	06-MAR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	394	ID	ABR77021 standard; protein; 266 AA.	DE	Human secreted polypeptide PRO180, SEQ ID NO:10.			
	US2003044927-A1.	PN						
	PD	06-MAR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	395	ID	ABM7778 standard; protein; 266 AA.	DE	Human secreted polypeptide PRO180, SEQ ID NO:10.			
	US20030404927-A1.	PN						
	PD	27-FEB-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	396	ID	ABR5829 standard; protein; 266 AA.	DE	Human secreted polypeptide PRO180, SEQ ID NO:10.			
	US2003040073-A1.	PN						
	PD	27-FEB-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	397	ID	ABO21762 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.			
	US2003054415-A1.	PN						
	PD	20-MAR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	398	ID	ABO19932 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.			
	US200303224-A1.	PN						
	PD	13-FEB-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	399	ID	ABO24235 standard; protein; 266 AA.	DE	Human secreted/transmembrane protein (PRO) #5.			
	US2003064467-A1.	PN						
	PD	03-APR-2003.						
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;		
	Best Local Similarity	100.0%;	Pred. No. 5e-149;					
RESULT	400	ID	ABR85984 standard; protein; 266 AA.	DE	Human secreted polypeptide PRO180, SEQ ID NO:10.			
	US2003049759-A1.	PN						

PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 401
 ID ABM1636 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003064455-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 402
 ID ABM1635 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003064465-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 403
 ID ABR89339 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003073170-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 404
 ID ABR12466 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003073176-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 405
 ID ABR05756 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003066717-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 406
 ID ABO1481 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003066728-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 407
 ID ABM02957 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068764-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 408
 ID ABM18935 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104550-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.
RESULT 409
 ID ABM19240 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104551-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003059884-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 420 ID ABR87204 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003058687-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 421 ID ABR12771 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200303186-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 422 ID ABM30525 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003064443-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 423 ID ABM24425 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200306444-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 424 ID ABQ29339 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003058697-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 425 ID ABO31169 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003058710-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 426 ID ABR14296 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003056686-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 427 ID ABM09721 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200303178-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 428 ID ABO38846 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US200305874-A1.

PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 429 ID ABM34611 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US200304538-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 430 ID ABO51087 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003049751-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 431 ID ABO03913 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003036158-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 432 ID ABO10883 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003036151-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 433 ID ABO53111 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003044806-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 434 ID ABR77626 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003040067-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 435 ID ABO23930 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003054456-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 436 ID ABR78936 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003040067-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 437 ID ABR9354 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054457-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;

PN US2003059883-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 439
 ID ABM7160 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003049764-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 440
 ID ABM89949 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003073177-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 441
 ID AD22146 standard; protein: 266 AA.
 DE Human secreted/transmembrane polypeptide PRO180.
 PN US2003040473-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 442
 ID ABM27475 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003064442-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 443
 ID ABM13076 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2103064450-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 444
 ID ABO1779 standard; protein: 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068731-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 445
 ID ABM13991 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068683-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 446
 ID ABM08196 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068754-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 447
 ID ABO4066 standard; protein: 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068881-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 448
 ID ABM71501 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003096351-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 449
 ID ABM33696 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003096358-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 450
 ID ABM20155 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104556-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 451
 ID ABO48647 standard; protein: 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003049756-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 452
 ID ABO22481 standard; protein: 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003017982-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 453
 ID ABR72712 standard; protein: 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003031612-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 454
 ID ABO15354 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003031612-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 455
 ID ABR85069 standard; protein: 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003040065-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 456
 ID ABO15049 standard; protein: 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003044919-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 457
 ID ABO17184 standard; protein: 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003040077-A1.

PD 27-FEB-2003. Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 458
 ID ABM17473 standard; protein; 266 AA. SEQ ID NO:10.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003044928-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 459
 ID ADA06312 standard; protein; 266 AA.
 DE Human secreted/transmembrane PRO polypeptide #6.
 PN US2003149638-A1.
 PD 13-MAR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 460
 ID ADA39005 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003059782-A1..
 PD 27-MAR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 461
 ID ABR85374 standard; protein; 266 AA. SEQ ID NO:10.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003049746-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 462
 ID ABM76940 standard; protein; 266 AA. SEQ ID NO:10.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054464-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 463
 ID ABQ28119 standard; protein; 266 AA. SEQ ID NO:10.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003064549-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 464
 ID ABM22900 standard; protein; 266 AA. SEQ ID NO:10.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068757-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 465
 ID ABM30220 standard; protein; 266 AA. SEQ ID NO:10.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068723-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 466
 ID ABM16180 standard; protein; 266 AA. SEQ ID NO:10.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068741-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 467
 ID ADB85575 standard; protein; 266 AA.

ID ABMM21375 standard; protein; 266 AA. SEQ ID NO:10.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068744-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 468
 ID ABML4906 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068766-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 469
 ID ABO40981 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068694-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 470
 ID ABO36711 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068715-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 471
 ID ABO37321 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003068726-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 472
 ID ABM75111 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104544-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 473
 ID ABM75111 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003104544-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 474
 ID ABO46146 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003049760-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 475
 ID ADA82445 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003049755-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;

DE Novel human secreted and transmembrane protein PRO180.
 PN US2003049735-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 477
 ID AB96031 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2003054403-A1.
 PD 20-MAR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 478
 ID ABM31745 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003058680-A1.
 PD 10-APR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 479
 ID ABM31135 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003058762-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 480
 ID ADBB85753 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US200305472-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 481
 ID ABM32050 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003058708-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 482
 ID ABM32355 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003056713-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 483
 ID ADBB8254 standard; protein; 266 AA.
 DE Human PRO180 protein.
 PN US2003056161-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 484
 ID ADBB8061 standard; protein; 266 AA.
 DE Human PRO180 protein.
 PN US2003056000-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 485
 ID ABM31440 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003056761-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match 100.0%; Pred. No. 5e-149;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 486
 ID ABM30830 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003068771-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003083473-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003045463-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 ID ADC57503 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2003027754-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 488
 ID ADC54867 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2003045463-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 489
 ID ADC11734 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003049681-A1.
 PD 13-MAR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 490
 ID ADC11734 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003049681-A1.
 PD 13-MAR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 491
 ID ADC06958 standard; protein; 266 AA.
 DE Human PRO180 protein.
 PN US2003060602-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 492
 ID ADC56156 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2003064375-A1.
 PD 03-APR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 493
 ID ADC17137 standard; protein; 266 AA.
 DE Mammalian PRO polypeptide (SeqID 2).
 PN US2003064375-A1.
 PD 03-APR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 494
 ID ADC07211 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US2003068647-A1.
 PD 10-APR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 495
 ID ADC11201 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.

PN US2003069403-A1.
 PD 10-APR-2003.
 Query Match 100.0%; Pred. No. 5e-149;
 Best Local Similarity 100.0%; Pred. No. 5e-149; Length 266;
 RESULT 496
 ID ADC14815 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003073208-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 497
 ID ADC52330 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003138882-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 498
 ID ADC14323 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003082546-A1.
 PD 01-MAY-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 499
 ID ADD07815 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003068633-A1.
 PD 10-APR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 500
 ID ADC81600 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2003083461-A1.
 PD 01-MAY-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 501
 ID ADD07222 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2002093298-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 502
 ID ADC82213 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2003059833-A1.
 PD 27-MAR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 503
 ID ADD05433 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003087376-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 504
 ID ADC78249 standard; protein; 266 AA.
 DE Human secreted protein SEQ ID NO:56.
 PN WO2003072761-A1.
 PD 04-SEP-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 505

ID ADD08393 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003073090-A1.
 PD 17-APR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 506
 ID ADD06642 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2002193100-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 507
 ID ADC82889 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2003059783-A1.
 PD 27-MAR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 508
 ID ADD54396 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2003077593-A1.
 PD 24-APR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 509
 ID ADD36006 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003105298-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 510
 ID ADD55954 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2003077594-A1.
 PD 24-APR-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 511
 ID ADD54392 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2002132253-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 512
 ID ADE26546 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003087304-A1.
 PD 08-MAY-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 513
 ID ADE26013 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003087305-A1.
 PD 08-MAY-2003.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 514
 ID ADF66350 standard; protein; 266 AA.
 DE Human PRO80 amino acid sequence SEQ ID NO:23.
 PN US2002198148-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 515
 ID ADG01007 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US200318059-A1.
 PD 24-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 516
 ID ADG08560 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180793-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 517
 ID ADG02478 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003207397-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 518
 ID ADG01185 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003207399-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 519
 ID ADG95360 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003207398-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 520
 ID ADP95181 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180795-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 521
 ID ADG12175 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003207392-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 522
 ID ADH24034 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180918-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 523
 ID ADH34060 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180858-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 524
 ID ADH24204 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.

DB Novel human secreted and transmembrane protein PRO180.
 PN US200318059-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 525
 ID ADH23864 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180519-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 526
 ID ADH08835 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003120735-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 527
 ID ADG85268 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180904-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 528
 ID ADH24544 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180907-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 529
 ID ADH37400 standard; protein; 266 AA.
 DE Human secreted and transmembrane protein PRO180.
 PN US2003181646-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 530
 ID ADH01989 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003180837-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 531
 ID ADH37570 standard; protein; 266 AA.
 DE Human secreted and transmembrane protein PRO180.
 PN US2003181648-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 532
 ID ADG85608 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180905-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;

PN US2003180914-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 534 ID ADH38498 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181643-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 535 ID ADH38498 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003180794-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 536 ID ADH29127 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180860-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 537 ID ADH27543 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180906-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 538 ID ADH37740 standard; protein; 266 AA.
 DE Human secreted and transmembrane protein PRO180.
 PN US2003181647-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 539 ID ADH37917 standard; protein; 266 AA.
 DE Human secreted and transmembrane protein PRO180.
 PN US2003181649-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 540 ID ADH57337 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180920-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 541 ID ADH53419 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181636-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 542 ID ADH53649 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181641-A1.

PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 543 ID ADH51985 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181638-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 544 ID ADH49840 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181639-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 545 ID ADI25350 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181636-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 546 ID ADH90143 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181638-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 547 ID ADI25520 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181669-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 548 ID ADH97694 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181672-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 549 ID ADI35204 standard; protein; 266 AA.
 DE Human PRO polypeptide #6.
 PN US2003050457-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 550 ID ADI03542 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181656-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Query Match Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 551 ID ADI1199 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003181666-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 561
 ID AD103372 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181654-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 553
 ID ADH98973 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181659-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 553
 ID ADH98374 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181707-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 555
 ID ADH11049 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003181682-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 556
 ID ADH11559 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003181684-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 557
 ID ADH98204 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181709-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 558
 ID ADH98544 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181708-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 559
 ID ADH98034 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181673-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 560
 ID AD105022 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180848-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 570
 ID ADH97881 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181666-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 569
 ID ADH97864 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181674-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 569
 ID ADH97822 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003190669-A1.
 PD 08-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
 Pred. No. 5e-149;

RESULT 570
 ID ADH97864 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003190669-A1.

ID ADI01944 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; Pred. No. 5e-149; Length 266;
RESULT 571
ID ADI03202 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; Pred. No. 5e-149; Length 266;
RESULT 572
ID ADI11389 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; Pred. No. 5e-149; Length 266;
RESULT 573
ID ADI02291 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; Pred. No. 5e-149; Length 266;
RESULT 574
ID ADI11729 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; Pred. No. 5e-149; Length 266;
RESULT 575
ID ADI05366 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; Pred. No. 5e-149; Length 266;
RESULT 576
ID ADH79438 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; Pred. No. 5e-149; Length 266;
RESULT 577
ID ADI19395 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; Pred. No. 5e-149; Length 266;
RESULT 578
ID ADI105196 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149; Pred. No. 5e-149; Length 266;
RESULT 579
ID ADI125860 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

PN US2003181671-A1.
 PD 25-SEP-2003
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 598
 ID ADK65372 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003191281-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 590
 ID ADH98714 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003191284-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC. .
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 591
 ID ADH9955 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003191287-A1.
 PA (GETH) GENENTECH INC. .
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 592
 ID ADL2616 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003207396-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 593
 ID ADM30150 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003073813-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 594
 ID ADJ3686 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003040013-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 595
 ID ADC52140 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003130483-A1.
 PD 10-JUL-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 596
 ID ADE4147 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003211572-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 597
 ID ADE4759 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003211574-A1.
 PD 13-NOV-2003.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149.
 RESULT 598
 ID ADG1399 standard; protein; 266 AA.
 DE Human PRO180 polypeptide.
 PN US2003194460-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149.
 RESULT 599
 ID ADG1399 standard; protein; 266 AA.
 DE Human PRO180 polypeptide.
 PN US2003228655-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149.
 RESULT 600
 ID ADP95972 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003215909-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149.
 RESULT 601
 ID ADG04243 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003215912-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149.
 RESULT 602
 ID ADG00403 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003215911-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149.
 RESULT 603
 ID ADH06572 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180852-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149.
 RESULT 604
 ID ADH06402 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180853-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149.
 RESULT 605
 ID ADG68823 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180855-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149.
 RESULT 606
 ID ADH27713 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180912-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149.
 RESULT 607

ID ADH25054 standard; protein; 266 AA.
 DE Human secreted and transmembrane protein PRO180.
 PN US2003180913-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 608
 ID ADH33686 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003181645-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 609
 ID ADG82659 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003215910-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 610
 ID ADH02329 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003180839-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 611
 ID ADH07936 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180845-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 612
 ID ADG69333 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180846-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 613
 ID ADH39154 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180917-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 614
 ID ADH25940 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003068770-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 615
 ID ADG83894 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003180842-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 616
 ID ADH19269 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.

DE Human secreted/transmembrane protein PRO180.
 PN US2003228656-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 617
 ID ADG85438 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003166848-A1.
 PD 04-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 618
 ID ADH06732 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180854-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 619
 ID ADH30063 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180856-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 620
 ID ADH24374 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180910-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 621
 ID ADH32209 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003068768-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 622
 ID ADG69503 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180844-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 623
 ID ADH07766 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180851-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 624
 ID ADG85778 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180861-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;

PN US2003180916-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 626
 ID ADH3516 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003181637-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 627
 ID ADH3556 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003181644-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 628
 ID ADH1066 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US200318038-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 629
 ID ADG69673 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180843-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 630
 ID ADH20762 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO180.
 PN US200324358-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 631
 ID ADH2159 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003180841-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 632
 ID ADG59163 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180847-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 633
 ID ADG5948 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180862-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 634
 ID ADH4884 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180909-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 635
 ID ADH39501 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180915-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 636
 ID ADH19802 standard; protein; 266 AA.
 DE Human secreted and transmembrane protein PRO180.
 PN US200319856-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 637
 ID ADH02499 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003180840-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 638
 ID ADG6893 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180849-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 639
 ID ADH07596 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180850-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 640
 ID ADG86118 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180853-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 641
 ID ADH24714 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180908-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 642
 ID ADH25762 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180911-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC. Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
 RESULT 643
 ID ADH3828 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180922-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 644
 ID ADH57167 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181642-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 645
 ID ADH52155 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180921-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 646
 ID ADH49521 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180857-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 647
 ID ADH90483 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181700-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 648
 ID AD11249 standard; protein; 266 AA.
 DE Human polypeptide #1.
 PN US2003181683-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 649
 ID ADH98884 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003190698-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 650
 ID AD10214 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003190699-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 651
 ID ADH9653 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181701-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 652
 ID ADH9648 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US200403321-A1.
 PD 05-FEB-2004.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;

Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 653
 ID ADJ98528 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003187197-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 654
 ID ADJ98598 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003187228-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 655
 ID ADH78857 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181703-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 656
 ID ADJ99091 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003186408-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 657
 ID ADJ99261 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003187196-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 658
 ID ADJ98879 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003187242-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 659
 ID ADH79027 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181702-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 660
 ID ADK000887 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003186407-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 661
 ID ADK14408 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003187229-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 662
 ID AEA38350 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein cDNA, #73.
 PN US2005112725-A1.
 PD 26-MAY-2005.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 56 .

RESULT 663
 ID ADM31315 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2004048334-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 56 .

RESULT 664
 ID ADM36362 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2004048335-A1.
 PD 19-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 56 .

RESULT 665
 ID ADM40167 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2004048335-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 56 .

RESULT 666
 ID ADM80857 standard; protein; 266 AA.
 DE Human polypeptide #1.
 PN US20040405841-A1.
 PD 25-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 56 .

RESULT 667
 ID ADN06777 standard; protein; 266 AA.
 DE Human secreted polypeptide #9.
 PN US2004038277-A1.
 PD 26-FEB-2004.
 PA (HUMA) HUMAN GENOME SCI INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 9 .

RESULT 668
 ID ADN17775 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane Protein PRO180.
 PN US2004091959-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 9 .

RESULT 669
 ID ADV77697 standard; protein; 266 AA.
 DE Neoplastic disease detection protein PRO180.
 PN US2005059102-A1.
 PD 17-MAR-2005.
 PA (EAT0 /) EATON D L.
 PA (FILV /) FILVAROFF E.
 PA (GRIM /) GRIMALDI J C.
 PA (GURN /) GURNEY A L.
 PA (WATA /) WATANABE C K.
 PA (WOOD /) WOOD W L.
 Query Match 100.0%; Score 1392; DB 9; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 9 .

RESULT 670
 ID AED11495 standard; protein; 266 AA.
 DE Human gene 26 encoded secreted protein HCPC191, SEQ ID NO: 56 .
 PN US2005214786-A1.
 PD 29-SEP-2005.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 100.0%; Score 1392; DB 9; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 56 .

RESULT 671
 ID AED50005 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2005163766-A1.
 PD 28-JUL-2005.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 9; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 56 .

RESULT 672
 ID AEF12528 standard; protein; 266 AA.
 DE Human PRO180 protein SEQ ID NO:2.
 PN US2006108901-A1.
 PD 12-JUN-2006.
 PA (AEF74217 standard; protein; 266 AA.
 DE Human PRO180 protein SEQ ID NO:2.
 PN US2005260647-A1.
 PD 24-NOV-2005.
 PA (EAT0 /) EATON D L.
 PA (FILV /) FILVAROFF E.
 PA (GRIM /) GRIMALDI J C.
 PA (GURN /) GURNEY A L.
 PA (WATA /) WATANABE C K.
 PA (WOOD /) WOOD W L.
 Query Match 100.0%; Score 1392; DB 10; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 10 .

RESULT 673
 ID AEF12528 standard; protein; 266 AA.
 DE Human PRO180 protein SEQ ID NO:2.
 PN US2006108901-A1.
 PD 12-JUN-2006.
 PA (AEF74217 standard; protein; 266 AA.
 DE Human PRO180 protein SEQ ID NO:2.
 PN US2005260647-A1.
 PD 24-NOV-2005.
 PA (EAT0 /) EATON D L.
 PA (FILV /) FILVAROFF E.
 PA (GRIM /) GRIMALDI J C.
 PA (GURN /) GURNEY A L.
 PA (WATA /) WATANABE C K.
 PA (WOOD /) WOOD W L.
 Query Match 100.0%; Score 1392; DB 10; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 10 .

RESULT 674
 ID AY27575 standard; protein; 267 AA.
 DE Human secreted protein encoded by gene No. 9 .
 PN WO924836-A1.
 PD 20-MAY-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 100.0%; Score 1392; DB 2; Length 267;
 Best Local Similarity 100.0%; Pred. No. 5e-149; SEQ ID NO: 2 .

RESULT 675
 ID ADG78386 standard; protein; 267 AA.
 DE Human secreted protein in #9.
 PN US2003211472-A1.
 PD 13-NOV-2003.
 PA (FENG /) FENG P.
 PA (RUBE /) RUBEN S M.
 PA (ROSE /) ROSEN C A.
 PA (EBNE /) EBNER R.
 PA (OLSE /) OLSEN H S.
 PA (NIJJ /) NI J.
 PA (WEIY /) WEI Y.
 PA (SCOPP /) SCOPET D R.
 PA (MOOR /) MOORE P A.
 PA (KYAW /) KYAW H.
 PA (LAFOL /) LAFOLUR D W.
 PA (SHIY /) SHI Y.
 PA (JIANA /) JANAT F.
 PA (ENDR /) ENDRESS G A.

PA (CART/) CARTER K C. 100.0%; Score 1392; DB 8; Length 267;
 Best Local Similarity 100.0%; Pred. No. 5e-149; .

RESULT 677
 ID ABB12041 standard; peptide; 275 AA.
 DE Human secreted protein homologue, SEQ ID NO:24111.
 PN WO200157188-A2.
 PD 09-AUG-2001.
 PA (HYSEQ-) HYSEQ INC.
 Query Match 100.0%; Score 1392; DB 4; Length 275;
 Best Local Similarity 100.0%; Pred. No. 5.2e-149; .

RESULT 678
 ID AAM41354 standard; protein; 275 AA.
 DE Human Polypeptide SEQ ID NO 62855.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSEQ-) HYSEQ INC.
 Query Match 100.0%; Score 1392; DB 4; Length 275;
 Best Local Similarity 100.0%; Pred. No. 5.2e-149; .

RESULT 679
 ID AAB87526 standard; protein; 266 AA.
 DE Human PRO180.
 PN WO200116318-A2.
 PD 08-MAR-2001.

PA (GBT) GENENTECH INC. 99.9%; Score 1390; DB 4; Length 266;
 Best Local Similarity 99.6%; Pred. No. 8.4e-149; .

RESULT 680
 ID AAY36185 standard; protein; 267 AA.
 DE Human secreted protein #57.
 PN WO9925025-A2.
 PD 27-MAY-1999.
 PA (GEST) GENSET.
 Query Match 99.7%; Score 1388; DB 2; Length 267;
 Best Local Similarity 99.6%; Pred. No. 1.4e-148; .

RESULT 681
 ID ADP194037 standard; protein; 267 AA.
 DE Novel human secreted protein-related protein sequence SeqID190.
 PN US2003144490-A1.
 PD 31-JUL-2003.
 PA (EDWA/) EDWARDS J D M.
 PA (DUCL/) DUCLETT A.
 PA (BOUG/) BOUGUERET L.
 PA (GBT) GENSET.
 Query Match 99.7%; Score 1388; DB 7; Length 267;
 Best Local Similarity 99.6%; Pred. No. 1.4e-148; .

RESULT 682
 ID ADP19446 standard; protein; 267 AA.
 DE Human secreted polypeptide #297.
 PN US2004110939-A1.
 PD 10-JUN-2004.
 PA (GEST) GENSET SA.
 Query Match 99.7%; Score 1388; DB 8; Length 267;
 Best Local Similarity 99.6%; Pred. No. 1.4e-148; .

RESULT 683
 ID AAY29866 standard; protein; 208 AA.
 DE Human secreted protein clone pe318_4.
 PN WO946287-A1.
 PD 16-SEP-1999.
 PA (GEMY) GENETICS INST INC.
 Query Match 77.4%; Score 1078; DB 2; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.6e-113; .

RESULT 684
 ID ABP75476 standard; protein; 166 AA.
 DE Human secretory polypeptide SPTM SEQ ID NO 660.
 PN WO200283876-A2.
 PD 24-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 58.6%; Score 816; DB 6; Length 166;
 Best Local Similarity 93.4%; Pred. No. 6.8e-84; .

RESULT 685
 ID AAB88330 standard; protein; 136 AA.
 DE Human membrane or secretory protein clone PSECC0031.
 PN EP1067182-A2.

PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST 52.1%; Score 725; DB 4; Length 136;
 Query Match 50.0%; Pred. No. 1.1e-73; .

Best Local Similarity 100.0%; Pred. No. 1.1e-73; .

RESULT 686
 ID ADY63025 standard; protein; 136 AA.
 DE Human clone PSECC0031 protein, SEQ ID 28.
 PN EP1514933-A1.
 PD 16-MAR-2005.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 52.1%; Score 725; DB 9; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.1e-73; .

RESULT 687
 ID AAY36138 standard; protein; 172 AA.
 DE Human secreted protein #10.
 PN WO9922825-A2.
 PD 27-MAY-1999.
 PA (GEST) GENSET.
 Query Match 42.8%; Score 595.5; DB 2; Length 172;
 Best Local Similarity 79.4%; Pred. No. 8e-59; .

RESULT 688
 ID ADJ45943 standard; protein; 172 AA.
 DE Novel human secreted protein-related protein sequence SeqID96.
 PN US2001144490-A1.
 PD 31-JUL-2003.
 PA (EDWA/) EDWARDS J D M.
 PA (DUCL/) DUCLETT A.
 PA (BOUG/) BOUGUERET L.
 Query Match 42.8%; Score 595.5; DB 7; Length 172;
 Best Local Similarity 79.4%; Pred. No. 8e-59; .

RESULT 689
 ID ADM04182 standard; protein; 238 AA.
 DE Human protein of the invention SEQ ID NO:2867.
 PN BP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 34.9%; Score 486.5; DB 7; Length 238;
 Best Local Similarity 38.6%; Pred. No. 3e-46; .

RESULT 690
 ID AEC87112 standard; protein; 238 AA.
 DE Human cDNA clone protein BRCOC20101230, SEQ ID 2867.
 PN EP1580263-A1.
 PD 28-SEP-2005.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 34.9%; Score 486.5; DB 9; Length 238;
 Best Local Similarity 38.6%; Pred. No. 3e-46; .

RESULT 691
 ID AAB26425 standard; protein; 231 AA.
 DE Human transmembrane protein (TMP)-11 protein.
 PN WO200234783-A2.
 PD 02-MAY-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 34.5%; Score 480.5; DB 5; Length 231;
 Best Local Similarity 38.7%; Pred. No. 1.4e-45; .

RESULT 692
 ID ADK70499 standard; protein; 231 AA.
 DE Respiratory disease differentially expressed protein #65.
 PN WO2003101233-A2.
 PD 11-DEC-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 34.5%; Score 480.5; DB 8; Length 231;
 Best Local Similarity 38.7%; Pred. No. 1.4e-45; .

RESULT 693
 ID AAB05342 standard; protein; 238 AA.
 DE Mouse secreted protein #1.
 PN WO20041192-A1.
 PD 05-JUL-2004.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 Query Match 34.4%; Score 479.5; DB 4; Length 238;
 Best Local Similarity 37.3%; Pred. No. 1.9e-45; .

RESULT 694
 ID ABO0065 standard; protein; 246 AA.
 DE Polypeptide encoded by novel human contig #116.

PN WO2003023013-A2.
 PD 20-MAR-2003.
 PA (HYSEB-) HYSEQ INC.
 Query Match 33.2%; Score 461.5; DB 6; Length 246;
 Best Local Similarity 39.3%; Pred. No. 2.2e-43;
 RESULT 695
 ID ABB60356 standard; protein; 246 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 7860.
 PN WO200111042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 26.0%; Score 361.5; DB 4; Length 246;
 Best Local Similarity 33.6%; Pred. No. 4.9e-32;
 RESULT 696
 ID AXY36219 standard; protein; 69 AA.
 DE Human secreted protein #91.
 PN WO92525-A2.
 PD 27-MAY-1999.
 PA (GEST) GENSET.
 Query Match 25.7%; Score 358; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 2.1e-32; Length 69;
 RESULT 697
 ID AAY336172 standard; protein; 69 AA.
 DE Human secreted protein #44.
 PN WO92585-A2.
 PD 27-MAY-1999.
 PA (GEST) GENSET.
 Query Match 25.7%; Score 358; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 2.1e-32;
 RESULT 698
 ID AD46071 standard; protein; 69 AA.
 DE Novel human secreted protein-related protein sequence SeqID224.
 PN US2003144490-A1.
 PD 31-JUL-2003.
 PA (EDWA/) EDWARDS J D M.
 (DUCL/) DUCLERT A.
 (BOUG/) BOUGUERET L.
 Query Match 25.7%; Score 358; DB 7; Length 69;
 Best Local Similarity 100.0%; Pred. No. 2.1e-32;
 RESULT 699
 ID AD45977 standard; protein; 69 AA.
 DE Novel human secreted protein-related protein sequence SeqID130.
 PN US2003144490-A1.
 PD 31-JUL-2003.
 PA (EDWA/) EDWARDS J D M.
 (DUCL/) DUCLERT A.
 (BOUG/) BOUGUERET L.
 Query Match 25.7%; Score 358; DB 7; Length 69;
 Best Local Similarity 100.0%; Pred. No. 2.1e-32;
 RESULT 700
 ID ADP19480 standard; protein; 69 AA.
 DE Human secreted polypeptide #331.
 PN US2004110939-A1.
 PD 10-JUN-2004.
 PA (GEST) GENSET SA.
 Query Match 25.7%; Score 358; DB 8; Length 69;
 Best Local Similarity 100.0%; Pred. No. 2.1e-32;
 RESULT 701
 ID ABG28122 standard; protein; 200 AA.
 DE Novel human diagnostic protein #28113.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSEB-) HYSEQ INC.
 Query Match 25.6%; Score 356.5; DB 4; Length 200;
 Best Local Similarity 74.0%; Pred. No. 1.4e-31;
 RESULT 702
 ID ABB57767 standard; protein; 85 AA.
 DE Human secretory polypeptide (SPTM)
 PN WO2002020756-A2.
 PD 14-MAR-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 23.6%; Score 356; DB 5; Length 85;
 Best Local Similarity 86.1%; Pred. No. 4.8e-32;

RESULT 703
 ID AAY01148 standard; protein; 69 AA.
 DE Human 5'; EST secreted protein SEQ ID NO:19.
 PN WO906439-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 1e-31;
 RESULT 704
 ID AAW93416 standard; protein; 69 AA.
 DE Human 5'; EST secreted protein clone 58-34-2-E7-FL2.
 PN WO906551-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 1e-31;
 RESULT 705
 ID AAY0166 standard; protein; 69 AA.
 DE Human 5'; EST secreted protein SEQ ID NO:19.
 PN WO906548-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 1e-31;
 RESULT 706
 ID AAY35882 standard; protein; 69 AA.
 DE Extended human secreted protein sequence, SEQ ID NO. 19.
 PN WO931236-A2.
 PD 24-JUN-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 1e-31;
 RESULT 707
 ID AAY59645 standard; protein; 69 AA.
 DE Secreted protein extended EST protein sequence #2.
 PN WO94018-A2.
 PD 12-AUG-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 1e-31;
 RESULT 708
 ID AAY01590 standard; protein; 69 AA.
 DE Secreted protein encoded by an extended 5' EST cDNA sequence.
 PN WO906554-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 1e-31;
 RESULT 709
 ID AAY12982 standard; protein; 69 AA.
 DE Human secreted protein encoded by 5' EST clone 58-34-2-E7-FL2.
 PN WO906552-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 1e-31;
 RESULT 710
 ID AAY2541 standard; protein; 69 AA.
 DE Human secreted protein 2 derived from extended cDNA.
 PN WO925025-A2.
 PD 27-MAY-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 1e-31;
 RESULT 711
 ID AAY12672 standard; peptide; 69 AA.
 DE Human 5'; EST secreted protein.
 PN WO906549-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 1e-31;
 RESULT 712

ID AAG00010 standard; protein; 69 AA.	DE Novel bronchial cancer-associated human protein SeqID836.
DB Human secreted protein #1.	PN DB10116701-A1.
PN EP1033401-A2.	PD 04-NOV-2004.
PD 06-SEP-2000.	PA (HINZ-) HINZMANN B.
PA (GEST-) GENSET.	PA (HERM-) HERMANN K.
Query Match 25.3%; Score 352; DB 3; Length 69;	PA (CAST-) HEIDEN CASTANOS-VELEZ E.
Best Local Similarity 98.5%; Pred. No. 1e-31;	Query Match 18.0%; Score 251; DB 8; Length 132;
RESULT 713	Best Local Similarity 33.3%; Pred. No. 7.4e-20;
ID AD73027 standard; protein; 69 AA.	RESULT 722
DE cDNA 58-34-2-E7-FL2-encoded secreted protein, SEQ ID NO:1.	ID ADS11008 standard; protein; 233 AA.
PN US6822072-B1.	DE Human therapeutic protein - SEQ ID 1245.
PD 23-NOV-2004.	PN WO2004080148-A2.
PA (GEST-) GENSET SA.	PD 23-SEP-2004.
Query Match 25.3%; Score 352; DB 8; Length 69;	PA (NUVBE-) NUVELLO INC.
Best Local Similarity 98.5%; Pred. No. 1e-31;	Query Match 15.8%; Score 220-5; DB 8; Length 233;
RESULT 714	Best Local Similarity 27.2%; Pred. No. 4.7e-16;
ID ABB8768 standard; protein; 180 AA.	RESULT 723
DE Human polypeptide SEQ ID NO 2144.	ID ABO00507 standard; protein; 283 AA.
PN WO200190304-A2.	DE Novel human polypeptide #94.
PD 29-NOV-2001.	PN WO2003023013-A2.
PA (HUMA-) HUMAN GENOME SCI INC.	PD 20-MAR-2003.
Query Match 22.8%; Score 317.5; DB 5; Length 180;	PA (HYSE-) HYSEQ INC.
Best Local Similarity 33.3%; Pred. No. 3.2e-27;	Query Match 15.4%; Score 214.5; DB 6; Length 283;
RESULT 715	Best Local Similarity 26.2%; Pred. No. 3e-15;
ID AAG812719 standard; protein; 114 AA.	RESULT 724
DE Human AFP protein sequence SEQ ID NO:76.	ID AAB08366 standard; protein; 249 AA.
PN WO200129221-A2.	DE Amino acid sequence of a human secretory protein.
PD 26-APR-2001.	PN WO200052151-A2.
PA (ZYMO-) ZYMOGENETICS INC.	PD 08-SEP-2000.
Query Match 19.6%; Score 272.5; DB 4; Length 114;	PA (INCY-) INCYTE PHARM INC.
Best Local Similarity 47.5%; Pred. No. 2.2e-22;	Query Match 15.2%; Score 212; DB 3; Length 249;
RESULT 716	Best Local Similarity 26.5%; Pred. No. 4.8e-15;
ID AAB93532 standard; protein; 132 AA.	RESULT 725
DE Human protein sequence SEQ ID NO:13115.	ID AAM38964 standard; protein; 249 AA.
PN EP1074617-A2.	DE Human polypeptide SEQ ID NO 2109.
PD 07-FEB-2001.	PN WO200153312-A1.
PA (HELI-) HELIX RES INST.	PD 26-JUL-2001.
Query Match 18.0%; Score 251; DB 4; Length 132;	PA (HYSE-) HYSEQ INC.
Best Local Similarity 33.3%; Pred. No. 7.4e-20;	Query Match 15.2%; Score 212; DB 4; Length 249;
RESULT 717	Best Local Similarity 26.5%; Pred. No. 4.8e-15;
ID ADL0520 standard; protein; 132 AA.	RESULT 726
DE Human tumour-associated antigenic target (TAT) polypeptide #19.	ID AAM51628 standard; protein; 249 AA.
PN WO2000016225-A2.	DE Human plasminogen activator inhibitor 2-27 polypeptide.
PD 26-FEB-2004.	PN CN1313331-A.
PA (GETH-) GENENTECH INC.	PD 19-SEP-2001.
Query Match 18.0%; Score 251; DB 8; Length 132;	PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Best Local Similarity 33.3%; Pred. No. 7.4e-20;	Query Match 15.2%; Score 212; DB 5; Length 249;
RESULT 718	Best Local Similarity 26.5%; Pred. No. 4.8e-15;
ID ADJ75472 standard; protein; 132 AA.	RESULT 727
DE Marker gene related amino acid sequence SEQ ID NO:724.	ID ADP18677 standard; protein; 249 AA.
PN EP139474-A2.	DE Human protein encoded by TAT41 cDNA used to treat cancer SeqID 37.
PD 03-MAR-2004.	PN WO2004045516-A2.
PA (GENO-) GENOX RES INC.	PD 03-JUN-2004.
Query Match 18.0%; Score 251; DB 8; Length 132;	PA (GETH-) GENENTECH INC.
Best Local Similarity 33.3%; Pred. No. 7.4e-20;	Query Match 15.2%; Score 212; DB 8; Length 249;
RESULT 719	Best Local Similarity 26.5%; Pred. No. 4.8e-15;
ID ADR14452 standard; protein; 132 AA.	RESULT 728
DE Human NF-kappaB pathway-associated protein SeqID453.	ID AAY12179 standard; protein; 36 AA.
PN WO2004046557-A2.	DE Human 5' EST secreted protein SEQ ID NO: 492.
PD 05-AUG-2004.	PN WO9905554-A2.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.	PD 11-FEB-1999.
Query Match 18.0%; Score 251; DB 8; Length 132;	PA (GEST-) GENSET.
Best Local Similarity 33.3%; Pred. No. 7.4e-20;	Query Match 14.0%; Score 195; DB 2; Length 36;
RESULT 720	Best Local Similarity 100.0%; Pred. No. 2.9e-14;
ID ADP24981 standard; protein; 132 AA.	RESULT 729
DE PRO polypeptide SEQ ID NO:2159.	ID AAM40750 standard; protein; 274 AA.
PN WO2004041170-A2.	DE Human polypeptide SEQ ID NO 5681.
PD 21-MAY-2004.	PN WO20053312-A1.
PA (GETH-) GENENTECH INC.	PD 26-JUL-2001.
Query Match 18.0%; Score 251; DB 8; Length 132;	PA (HYSE-) HYSEQ INC.
Best Local Similarity 33.3%; Pred. No. 7.4e-20;	Query Match 13.8%; Score 192.5; DB 4; Length 274;
RESULT 721	Best Local Similarity 31.4%; Pred. No. 9e-13;
ID ADU06610 standard; protein; 132 AA.	RESULT 730

ID ABG17213 standard; protein; 308 AA.
DE Novel human diagnostic protein #17204.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSSQ INC. Query Match 12.9%; Score 180; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 731
ID ABG16460 standard; protein; 466 AA.
DE Novel human diagnostic protein #16451.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSSQ INC. Query Match 12.7%; Score 176.5; DB 4; Length 466;
Best Local Similarity 60.0%; Pred. No. 1.2e-10;
RESULT 732
ID AAB00331 standard; protein; 253 AA.
DE Human membrane-bound protein-60 alternative mature protein sequence.
PN WO20013567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC. Query Match 11.5%; Score 160.5; DB 4; Length 253;
Best Local Similarity 24.5%; Pred. No. 3.5e-09;
RESULT 733
ID AAB00331 standard; protein; 256 AA.
DE Human membrane-bound protein-60 (Zsig60) mature protein sequence.
PN WO20013567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC. Query Match 11.5%; Score 160.5; DB 4; Length 256;
Best Local Similarity 24.5%; Pred. No. 3.5e-09;
RESULT 734
ID AAB18985 standard; protein; 271 AA.
DE Amino acid sequence of a human transmembrane protein.
PN WO20056891-A2.
PD 28-SEP-2000.
PA (INCY-) INCYTE PHARM INC. Query Match 11.5%; Score 160.5; DB 3; Length 271;
Best Local Similarity 24.5%; Pred. No. 3.8e-09;
RESULT 735
ID AAB00330 standard; protein; 271 AA.
DE Human membrane-bound protein-60 (Zsig60).
PN WO20013567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC. Query Match 11.5%; Score 160.5; DB 4; Length 271;
Best Local Similarity 24.5%; Pred. No. 3.8e-09;
RESULT 736
ID AAY48244 standard; protein; 304 AA.
DE Human prostate cancer-associated protein 30.
PN DE19811193-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH. Query Match 10.9%; Score 152; DB 2; Length 304;
Best Local Similarity 24.0%; Pred. No. 4.1e-08;
RESULT 737
ID AAB00334 standard; protein; 160 AA.
DE Human membrane-bound protein-60 alternative mature extracellular portion.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC. Query Match 10.9%; Score 151.5; DB 4; Length 160;
Best Local Similarity 29.5%; Pred. No. 1.9e-08;
RESULT 738
ID AAB00333 standard; protein; 163 AA.
DE Human membrane-bound protein-60 (Zsig60) mature extracellular portion.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC. Query Match 10.9%; Score 151.5; DB 4; Length 163;
Best Local Similarity 29.5%; Pred. No. 2e-08;
RESULT 739
ID AAY94930 standard; protein; 437 AA.

DE Human secreted protein clone qal35_1 protein sequence SEQ ID NO:66.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC. Query Match 10.9%; Score 151.5; DB 3; Length 437;
Best Local Similarity 26.8%; Pred. No. 7.7e-08;
RESULT 740
ID AAY95013 standard; protein; 178 AA.
DE Human secreted protein vc48_1, SEQ ID NO:66.
PN WO20011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC. Query Match 10.6%; Score 147.5; DB 3; Length 178;
Best Local Similarity 24.9%; Pred. No. 6.4e-08;
RESULT 741
ID ADN02727 standard; protein; 255 AA.
DE Human receptor and membrane -associated protein #30.
PN WO2004029218-A2.
PD 08-APR-2004.
PA (INCY-) INCYTE CORP. Query Match 10.5%; Score 146.5; DB 8; Length 255;
Best Local Similarity 24.6%; Pred. No. 1.4e-07;
RESULT 742
ID ABO00615 standard; protein; 63 AA.
DE Novel human polypeptide #202.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC. Query Match 9.1%; Score 126; DB 6; Length 63;
Best Local Similarity 47.2%; Pred. No. 4.2e-06;
RESULT 743
ID ADS1.1007 standard; protein; 127 AA.
DE Human therapeutic protein - SEQ ID 1244.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC. Query Match 8.8%; Score 122.5; DB 8; Length 127;
Best Local Similarity 32.1%; Pred. No. 2.8e-05;
RESULT 744
ID AAY04149 standard; peptide; 21 AA.
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.
PN WO906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET. Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
RESULT 745
ID AAY11369 standard; protein; 21 AA.
DE Human 5' EST secreted protein SEQ ID NO:20.
PN WO906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET. Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
RESULT 746
ID AAY12516 standard; peptide; 21 AA.
DE Human 5' EST signal peptide SEQ ID NO: 20 from WO 9906553.
PN WO9906553-A2.
PD 11-FEB-1999.
PA (GEST) GENSET. Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
RESULT 747
ID AAY3583 standard; peptide; 21 AA.
DE Signal peptide of extended secreted protein, SEQ ID NO. 20.
PN WO931136-A2.
PD 24-JUN-1999.
PA (GEST) GENSET. Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
RESULT 748
ID AAY59644 standard; peptide; 21 AA.
DE Secreted protein extended EST signal peptide #2.

RESULT 757
 ID ADUT1405 standard; peptide; 21 AA.
 DE CDNA 58-34-2-E7-FL2-encoded secretory signal peptide, SEQ ID NO:2.
 PN US6822072-B1.
 PD 23-NOV-2004.
 PA (GEST) GENSET SA.
 Query Match Similarity 100.0%; Score 118; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 749
 ID AAY25452 standard; peptide; 21 AA.
 DE Human secreted protein 2 signal peptide derived from extended cDNA.
 PN WO928825-A2.
 PD 27-MAY-1999.
 PA (GEST) GENSET.
 Query Match Similarity 8.5%; Score 118; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 750
 ID AAY12671 standard; peptide; 21 AA.
 DE Human 5' EST secreted protein signal peptide.
 PN WO90549-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match Similarity 8.5%; Score 118; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 751
 ID AAY11711 standard; protein; 21 AA.
 DE Peptide encoded by extended cDNA derived from 5' EST.
 PN WO900550-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match Similarity 8.5%; Score 118; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 752
 ID AAY64644 standard; peptide; 21 AA.
 DE Human 58-34-2-E7-FL2 signal peptide.
 PN WO953051-A2.
 PD 21-OCT-1999.
 PA (GEST) GENSET.
 Query Match Similarity 8.5%; Score 118; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 753
 ID AAG00011 standard; peptide; 21 AA.
 DE Human secreted protein #1 signal peptide.
 PN EP10334-A2.
 PD 06-SEP-2000.
 PA (GEST) GENSET.
 Query Match Similarity 8.5%; Score 118; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 754
 ID AAO2028 standard; peptide; 21 AA.
 DE Signal peptide encoded by the cDNA 58-34-2-E7-FL2.
 PN CA234602-A1.
 PD 18-OCT-2001.
 PA (GEST) GENSET.
 Query Match Similarity 8.5%; Score 118; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 755
 ID ADJ45867 standard; peptide; 21 AA.
 DE Novel human secreted protein-related peptide sequence SeqID20.
 PN US2003144490-A1.
 PD 31-JUL-2003.
 PA (EDWA/) EDWARDS J D M.
 PA (DUCL/) DUCLBERT A.
 PA (BOUG/) BOUGUERET L.
 Query Match Similarity 8.5%; Score 118; DB 7; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 756
 ID ADM77739 standard; peptide; 21 AA.
 DE Signal sequence #12.
 PN US2003162176-A1.
 PD 28-AUG-2003.
 PA (EDWA/) EDWARDS J D M.
 PA (DUCL/) DUCLBERT A.
 PA (BOUG/) BOUGUERET L.
 Query Match Similarity 8.5%; Score 118; DB 7; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;

RESULT 757
 ID ADZB9199 standard; peptide; 21 AA.
 DE Signal peptide from secreted protein encoded by extended EST cDNA #2.
 PN US2005106599-A1.
 PD 19-MAY-2005.
 PA (BOUG/) BOUGUERET L.
 PA (EDWA/) EDWARDS J D M.
 PA (DUCL/) DUCLBERT A.
 Query Match Similarity 8.5%; Score 118; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 758
 ID ADZB9199 standard; peptide; 21 AA.
 DE Human 5' EST encoded signal peptide SEQ ID NO:2.
 PN US2005106595-A1.
 PD 19-MAY-2005.
 PA (GEST) GENSET SA.
 Query Match Similarity 8.5%; Score 118; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 759
 ID ADZB2396 standard; peptide; 21 AA.
 DE Human 5' EST encoded signal peptide SEQ ID NO:2.
 PN US2005106595-A1.
 PD 19-MAY-2005.
 PA (GEST) GENSET SA.
 Query Match Similarity 8.5%; Score 118; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 RESULT 760
 ID AAY04167 standard; peptide; 21 AA.
 DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.
 PN WO906548-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match Similarity 8.1%; Score 113; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 2.8e-05;
 RESULT 761
 ID AAU04087 standard; peptide; 21 AA.
 DE Signal peptide encoded by Human cDNA 58-34-2-E7-FL2.
 PN EP104808-A1.
 PD 06-JUN-2001.
 PA (GEST) GENSET.
 Query Match Similarity 8.1%; Score 113; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 RESULT 762
 ID ABB60233 standard; protein; 275 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 7491.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match Similarity 7.7%; Score 106.5; DB 4; Length 275;
 Best Local Similarity 21.3%; Pred. No. 0.0033;
 RESULT 763
 ID AAB38199 standard; peptide; 220 AA.
 DE Fragment of human secreted protein encoded by gene 53 clone HFABG18.
 PN WO200061623-A1.
 PD 19-OCT-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Similarity 7.5%; Score 105; DB 3; Length 220;
 Best Local Similarity 22.8%; Pred. No. 0.0057;
 RESULT 764
 ID AAM93195 standard; protein; 218 AA.
 DE Human polypeptide, SEQ ID NO: 2575.
 PN EP110094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HBLIX RES INST.
 Query Match Similarity 7.3%; Score 101; DB 4; Length 218;
 Best Local Similarity 22.8%; Pred. No. 0.016;
 RESULT 765
 ID ADL30542 standard; protein; 218 AA.
 DE Human protein encoded by a full length cDNA clone SeqID 2575.
 PN EP139545-A2.
 PD 10-MAR-2004.
 PA (REAS-) RBS ASSOC BIOTECHNOLOGY.
 Query Match Similarity 7.3%; Score 101; DB 8; Length 218;

Best Local Similarity 22.8%; Pred. No. 0.016;
RESULT 766
 ID AEB38816 standard; protein; 581 AA.
 DE L. pneumophila protein SEQ ID NO 3148.
 PN WO2005049642-A2.
 PD 02-JUN-2005.
 PA (INSP) INST PASTEUR.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (IUYL-) UNIV LYON 1 BERNARD CLAUDE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 7.1%; Score 99.5; DB 9; Length 581;
 Best Local Similarity 24.4%; Pred. No. 0.092;
RESULT 767
 ID ADM06102 standard; protein; 187 AA.
 DE Human Protein of the invention SEQ ID NO:4787.
 PN EP1347946-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 7.1%; Score 99; DB 7; Length 187;
 Best Local Similarity 23.4%; Pred. No. 0.022;
RESULT 768
 ID ABC89012 standard; protein; 187 AA.
 DE Human cDNA clone protein TRACH20128110, SEQ ID 4787.
 PN EP1580063-A1.
 PD 28-SEP-2005.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 7.1%; Score 99; DB 9; Length 187;
 Best Local Similarity 23.4%; Pred. No. 0.022;
RESULT 769
 ID ABU4347 standard; protein; 1066 AA.
 DE Protein encoded by Prokaryotic essential gene #30874.
 PN WO200271183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 7.1%; Score 98.5; DB 6; Length 1066;
 Best Local Similarity 19.5%; Pred. No. 0.28;
RESULT 770
 ID ABU47563 standard; protein; 1120 AA.
 DE Protein encoded by Prokaryotic essential gene #33090.
 PN WO200271183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 7.1%; Score 98.5; DB 6; Length 1120;
 Best Local Similarity 19.5%; Pred. No. 0.3;
RESULT 771
 ID ABU46980 standard; protein; 1120 AA.
 DE Protein encoded by Prokaryotic essential gene #32507.
 PN WO200271183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 7.1%; Score 98.5; DB 6; Length 1120;
 Best Local Similarity 19.5%; Pred. No. 0.3;
RESULT 772
 ID AEP42187 standard; protein; 268 AA.
 DE L. pneumophila protein SEQ ID NO 6519.
 PN WO200409642-A2.
 PD 02-JUN-2005.
 PA (INSP) INST PASTEUR.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (IUYL-) UNIV LYON 1 BERNARD CLAUDE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.8%; Score 94.5; DB 9; Length 268;
 Best Local Similarity 22.6%; Pred. No. 0.12;
RESULT 773
 ID AEB19048 standard; protein; 291 AA.
 DE L. pneumophila protein SEQ ID NO 3380.
 PN WO2005049642-A2.
 PD 02-JUN-2005.
 PA (INSP) INST PASTEUR.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (IUYL-) UNIV LYON 1 BERNARD CLAUDE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.8%; Score 94.5; DB 9; Length 291;

Best Local Similarity 22.6%; Pred. No. 0.13;
RESULT 774
 ID ABU34113 standard; protein; 548 AA.
 DE Protein encoded by Prokaryotic essential gene #19640.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.8%; Score 94.5; DB 6; Length 548;
 Best Local Similarity 18.2%; Pred. No. 0.31;
RESULT 775
 ID ABU39811 standard; protein; 269 AA.
 DE Protein encoded by Prokaryotic essential gene #25338.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.8%; Score 94; DB 6; Length 269;
 Best Local Similarity 21.7%; Pred. No. 0.13;
RESULT 776
 ID AEC57250 standard; protein; 452 AA.
 DE L. acidophilus maltose ABC transporter permease SEQ ID 64.
 PN WO2005084411-A2.
 PD 15-SEP-2005.
 PA (UNNC-) UNIV NORTH CAROLINA STATE.
 Query Match 6.8%; Score 94; DB 9; Length 452;
 Best Local Similarity 19.2%; Pred. No. 0.27;
RESULT 777
 ID AAG44537 standard; protein; 303 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 55801.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (UNNC-) UNIV NORTH CAROLINA STATE.
 Query Match 6.7%; Score 93.5; DB 3; Length 303;
 Best Local Similarity 21.8%; Pred. No. 0.18;
RESULT 778
 ID AAG44536 standard; protein; 367 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 55800.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (UNNC-) UNIV NORTH CAROLINA STATE.
 Query Match 6.7%; Score 93.5; DB 3; Length 303;
 Best Local Similarity 21.8%; Pred. No. 0.24;
RESULT 779
 ID ABU15091 standard; protein; 1120 AA.
 DE Protein encoded by Prokaryotic essential gene #618.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.7%; Score 93; DB 6; Length 1120;
 Best Local Similarity 19.6%; Pred. No. 1.2;
RESULT 780
 ID ABU47616 standard; protein; 473 AA.
 DE Protein encoded by Prokaryotic essential gene #33143.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.6%; Score 92.5; DB 6; Length 473;
 Best Local Similarity 22.8%; Pred. No. 0.43;
RESULT 781
 ID ABB89477 standard; protein; 118 AA.
 DE Human polypeptide SEQ ID NO 1853.
 PN WO200190304-A2.
 PD 29-NOV-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 6.6%; Score 91.5; DB 5; Length 118;
 Best Local Similarity 28.0%; Pred. No. 0.083;
RESULT 782
 ID ADC94520 standard; protein; 291 AA.
 DE E. faecium protein sequence SEQ ID 4147.
 PN US6583275-B1.
 PD 24-JUN-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.6%; Score 91.5; DB 7; Length 291;
 Best Local Similarity 22.9%; Pred. No. 0.29;
RESULT 783
 ID ADN23444 standard; protein; 373 AA.

DE Bacterial polypeptide #6097.
 PN US200333675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 6.6%; Score 91.5; DB 8; Length 373;
 Best Local Similarity 23.0%; Pred. No. 0.41;
 RESULT 784
 ID AAU03808 standard; protein; 387 AA.
 DE G protein-coupled receptor-like (GPCR-like) receptor protein #7.
 PN WO200118533-A2.
 PD 31-MAY-2001.
 PA (PHAA) PHARMACIA & UPJOHN
 Query Match 6.6%; Score 91.5; DB 4; Length 387;
 Best Local Similarity 23.0%; Pred. No. 0.43;
 RESULT 785
 ID ABB91319 standard; protein; 712 AA.
 DE Herbicidally active polypeptide SEQ ID NO 1150.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 6.6%; Score 91.5; DB 5; Length 712;
 Best Local Similarity 22.2%; Pred. No. 0.99;
 RESULT 786
 ID ADX68404 standard; protein; 486 AA.
 DE Plant full length insert polypeptide seqid 39247.
 PN US200434888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREBN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match 6.5%; Score 91; DB 8; Length 486;
 Best Local Similarity 22.6%; Pred. No. 0.67;
 RESULT 787
 ID ADX87645 standard; protein; 486 AA.
 DE Plant full length insert polypeptide seqid 50309.
 PN US200434888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREBN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match 6.5%; Score 91; DB 8; Length 486;
 Best Local Similarity 22.6%; Pred. No. 0.67;
 RESULT 788
 ID ADY12322 standard; protein; 487 AA.
 DE Plant full length insert polypeptide seqid 68137.
 PN US200434888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREBN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match 6.5%; Score 91; DB 8; Length 487;
 Best Local Similarity 22.6%; Pred. No. 0.67;
 RESULT 789
 ID ADN46319 standard; protein; 451 AA.
 DE Thermococcus kodakarensis KODI protein sequence SeqID217.
 PN WO200422736-A1.
 PD 18-MAR-2004.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match 6.5%; Score 90.5; DB 8; Length 451;
 Best Local Similarity 21.2%; Pred. No. 0.68;

RESULT 790
 ID AAB76803 standard; protein; 283 AA.
 DE Corynebacterium glutamicum MCT protein SEQ ID NO:588.
 PN WO200100805-A2.
 PD 04-JAN-2001.
 PA (BADI) BASF AG.
 Query Match 6.5%; Score 90; DB 4; Length 283;
 Best Local Similarity 23.8%; Pred. No. 0.41;
 RESULT 791
 ID AAG89779 standard; protein; 283 AA.
 DE C glutamicum protein fragment SEQ ID NO: 3533.
 PN EP108790-A2.
 PD 20-JUN-2001.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Query Match 6.5%; Score 90; DB 4; Length 283;
 Best Local Similarity 23.8%; Pred. No. 0.41;
 RESULT 792
 ID ABD46975 standard; protein; 283 AA.
 DE Membrane construction and membrane transport protein SEQ ID 252.
 PN US2005244935-A1.
 PD 03-NOV-2005.
 PA (BADI) BASF AG.
 Query Match 6.5%; Score 90; DB 9; Length 283;
 Best Local Similarity 23.8%; Pred. No. 0.41;
 RESULT 793
 ID ABD46977 standard; protein; 283 AA.
 DE Membrane construction and membrane transport protein SEQ ID 254.
 PN US2005244935-A1.
 PD 03-NOV-2005.
 PA (BADI) BASF AG.
 Query Match 6.5%; Score 90; DB 9; Length 283;
 Best Local Similarity 23.8%; Pred. No. 0.41;
 RESULT 794
 ID ADP98065 standard; protein; 505 AA.
 DE C. albicans specific gene, orf6_4442, protein sequence.
 PN WO2004056965-A2.
 PD 08-JUL-2004.
 PA (ELIT-) ELITRA PHARM INC.
 PA (ELIT-) ELITRA CANADA LTD.
 Query Match 6.5%; Score 90; DB 8; Length 505;
 Best Local Similarity 20.5%; Pred. No. 0.91;
 RESULT 795
 ID ABU45537 standard; protein; 458 AA.
 DE Protein encoded by Prokaryotic essential gene #31064.
 PN WO200271183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.5%; Score 89.5; DB 6; Length 458;
 Best Local Similarity 22.8%; Pred. No. 0.91;
 RESULT 796
 ID ABP26393 standard; protein; 579 AA.
 DE Streptococcus polypeptide SEQ ID NO 1962.
 PN WO200234771-A2.
 PD 02-MAY-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Query Match 6.4%; Score 89.5; DB 5; Length 579;
 Best Local Similarity 24.8%; Pred. No. 1.3;
 RESULT 797
 ID ADV88015 standard; protein; 579 AA.
 DE (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.4%; Score 89.5; DB 8; Length 579;
 Best Local Similarity 24.8%; Pred. No. 1.3;
 DE Streptococcus agalactiae protein sequence, SEQ ID 1209.
 PN FR2824074-A1.
 PD 31-OCT-2002.
 ID ADV22204 standard; protein; 579 AA.
 DE Streptococcus agalactiae protein, SEQ ID 3345.
 PN WO200292818-A2.
 PD 21-NOV-2002.
 PA (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI. Query Match 6.4%; Score 89.5; DB 8; Length 579;
 Best Local Similarity 24.8%; Pred. No. 1.3%;
RESULT 799
 ID ADV0068 standard; protein; 579 AA.
 DE Streptococcus agalactiae protein, SEQ ID 1209.
 PN WO20022818-A2.
 PD 21-NOV-2002.
 PA (INSP) INST PASTEUR.
 (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.4%; Score 89.5; DB 8; Length 579;
 Best Local Similarity 24.8%; Pred. No. 1.3%;
RESULT 800
 ID ABU50406 standard; protein; 428 AA.
 DE Protein encoded by Prokaryotic essential gene #35933.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.4%; Score 89; DB 6; Length 428;
 Best Local Similarity 21.6%; Pred. No. 0.94;
RESULT 801
 ID AAB94639 standard; protein; 637 AA.
 DE Human protein sequence SEQ ID NO:15654.
 PN EP1074417-A2.
 PD 07-FEB-2001.
 PA (HELIX- HELIX RES INST. (ELIT-) ELITRA PHARM INC. (INSP) INST PASTEUR.
 Query Match 6.4%; Score 89; DB 4; Length 637;
 Best Local Similarity 21.5%; Pred. No. 1.6;
RESULT 802
 ID ABU23408 standard; protein; 642 AA.
 DE Protein encoded by Prokaryotic essential gene #8935.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.4%; Score 89; DB 6; Length 642;
 Best Local Similarity 20.8%; Pred. No. 1.6;
RESULT 803
 ID AAU03497 standard; protein; 757 AA.
 DE Human steroid sensing domain protein.
 PN WO0016227-A2.
 PD 28-JUN-2001.
 PA (UZYU- UNIV ZURICH. (INCY-) INCYTE GENOMICS INC. (HELI-) HELIX RES INST. (REPS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 6.4%; Score 89; DB 4; Length 757;
 Best Local Similarity 21.5%; Pred. No. 2.1;
RESULT 804
 ID AAU41293 standard; protein; 758 AA.
 DE Human ORF1057 polypeptide sequence SEQ ID NO:2114.
 PN WO2000058473-A2.
 PD 05-OCT-2000.
 PA (CURAGEN CORP. (CURA-) CURAGEN CORP. (INCY-) INCYTE GENOMICS INC. (HELI-) HELIX RES INST. (REPS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 6.4%; Score 89; DB 3; Length 758;
 Best Local Similarity 21.5%; Pred. No. 2.1;
RESULT 805
 ID AAU74820 standard; protein; 1124 AA.
 DE Human RBPTR 3 protein.
 PN WO00198354-A2.
 PD 27-DEC-2001.
 PA (ELIT-) ELITRA PHARM INC. (AMCY) AMERICAN CYANAMID CO. (ELIT-) ELITRA PHARM INC.
 Query Match 6.4%; Score 89; DB 5; Length 1124;
 Best Local Similarity 21.5%; Pred. No. 3.6;
RESULT 806
 ID ADAS5083 standard; protein; 1203 AA.
 DE Human protein, SEQ ID 2651.
 PN EP1293559-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST. (REPS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 6.4%; Score 89; DB 6; Length 1203;
 Best Local Similarity 21.5%; Pred. No. 3.9;
RESULT 807
 ID ABG31547 standard; protein; 1330 AA.
 DE Human patched-like protein.
 PN WO200246402-A2.

PD 13-JUN-2002.
 PA (FARB) BAYER AG. Query Match 6.4%; Score 89; DB 5; Length 1330;
 Best Local Similarity 21.5%; Pred. No. 4.5;
RESULT 808
 ID AEB40780 standard; protein; 361 AA.
 DE L. pneumophila protein SEQ ID NO 5112.
 PN WO2005049642-A2.
 PD 02-JUN-2005.
 PA (INSP) INST PASTEUR.
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INRY) UNIV LYON 1 BERNARD CLAUDE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.4%; Score 88.5; DB 9; Length 361;
 Best Local Similarity 20.9%; Pred. No. 0.85;
RESULT 809
 ID ADY10982 standard; protein; 372 AA.
 DE Plant full length insert polypeptide seqid 66797.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LILINU-) LIJU J.
 PA (ZHOU-) ZHOU Y.
 PA (KOVALIC-) KOVALIC D K.
 PA (SCRE-) SCREEN S E.
 PA (TABATA-) TABASKA J E.
 PA (CAOY-) CAO Y.
 Query Match 6.4%; Score 88.5; DB 8; Length 372;
 Best Local Similarity 19.3%; Pred. No. 0.89;
RESULT 810
 ID AEB37466 standard; protein; 374 AA.
 DE L. pneumophila protein SEQ ID NO 1798.
 PN WO2005049642-A2.
 PD 02-JUN-2005.
 PA (INSP) INST PASTEUR.
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INRY) UNIV LYON 1 BERNARD CLAUDE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.4%; Score 88.5; DB 9; Length 374;
 Best Local Similarity 20.8%; Pred. No. 0.89;
RESULT 811
 ID AAB96747 standard; protein; 430 AA.
 DE Putative P. abyssi permease #26.
 PN FR2792651-A1.
 PD 27-OCT-2000.
 PA (IFRE-) IFREMER INST RECH EXPL MER.
 (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.4%; Score 88.5; DB 4; Length 430;
 Best Local Similarity 23.8%; Pred. No. 1.1;
RESULT 812
 ID AAR37309 standard; protein; 1165 AA.
 DE Cardiac adenylyl cyclase.
 PN EP543137-A1.
 PD 26-MAY-1993.
 PA (AMCY) AMERICAN CYANAMID CO. (ELIT-) ELITRA PHARM INC.
 Query Match 6.3%; Score 88; DB 2; Length 1165;
 Best Local Similarity 20.5%; Pred. No. 4.9;
RESULT 813
 ID ABU19057 standard; protein; 233 AA.
 DE Protein encoded by Prokaryotic essential gene #4624.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.3%; Score 87.5; DB 6; Length 233;
 Best Local Similarity 22.8%; Pred. No. 0.6;
RESULT 814
 ID ADD7113 standard; protein; 322 AA.
 DE Homogenotiseur peptyl transferase.
 PN WO2003080647-A2.
 PD 02-OCT-2003.
 PA (MONS) MONSANTO TECHNOLOGY LLC. (ELIT-) ELITRA PHARM INC.
 Query Match 6.3%; Score 87.5; DB 7; Length 322;
 Best Local Similarity 22.6%; Pred. No. 0.94;
RESULT 815

ID ADC77581 standard; protein; 453 AA.
DB Mouse tRNA amino acid sequence.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 6.3%; Score 87.5; DB 7; Length 453;
Best Local Similarity 19.9%; Pred. No. 1.5;
RESULT 816
ID ADS28619 standard; protein; 482 AA.
DE Bacterial polypeptide #17652.
PN US2003333675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKIS G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 86.5; DB 8; Length 400;
Best Local Similarity 21.9%; Pred. No. 1.7;
RESULT 817
ID ABB38011 standard; protein; 521 AA.
DE L. pneumophila protein SEQ ID NO 23731.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.3%; Score 87.5; DB 9; Length 521;
Best Local Similarity 22.1%; Pred. No. 1.6;
RESULT 818
ID ABB41315 standard; protein; 521 AA.
DE L. pneumophila protein SEQ ID NO 5667.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.3%; Score 87.5; DB 9; Length 521;
Best Local Similarity 22.5%; Pred. No. 1.8;
RESULT 819
ID ABB41995 standard; protein; 535 AA.
DE L. pneumophila protein SEQ ID NO 63227.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.2%; Score 87; DB 9; Length 535;
Best Local Similarity 26.0%; Pred. No. 2.2;
RESULT 820
ID ABU33543 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #19070.
PN WO200207183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86.5; DB 6; Length 239;
Best Local Similarity 20.4%; Pred. No. 0.81;
RESULT 821
ID ADT05651 standard; protein; 261 AA.
DE Haemophilus influenzae (NTthi) protein - SEQ ID 697.
PN WO2004078949-A2.
PD 16-SEP-2004.
PA (CHIL-) CHILDRENS HOSPITAL INC.
Query Match 6.2%; Score 86.5; DB 8; Length 261;
Best Local Similarity 24.2%; Pred. No. 0.92;
RESULT 822
ID ADH8729 standard; protein; 356 AA.
DE Enterococcus faecalis polypeptide #1509.
PN US6617156-B1.
PD 09-SEP-2003.

PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.2%; Score 86.5; DB 7; Length 356;
Best Local Similarity 19.2%; Pred. No. 1.4;
RESULT 823
ID ADS44642 standard; protein; 400 AA.
DE Bacterial polypeptide #23072.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 86.5; DB 8; Length 400;
Best Local Similarity 21.9%; Pred. No. 1.7;
RESULT 824
ID ABB47717 standard; protein; 583 AA.
DE Listeria monocytogenes protein #421.
PN WO20017335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.2%; Score 86.5; DB 5; Length 583;
Best Local Similarity 19.4%; Pred. No. 2.8;
RESULT 825
ID AAG39112 standard; protein; 1346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48347.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 86.5; DB 3; Length 1346;
Best Local Similarity 18.2%; Pred. No. 8.8;
RESULT 826
ID AAG39111 standard; protein; 1390 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48346.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 86.5; DB 3; Length 1390;
Best Local Similarity 18.2%; Pred. No. 9.2;
RESULT 827
ID AAG39110 standard; protein; 1403 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48345.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 86.5; DB 3; Length 1403;
Best Local Similarity 18.2%; Pred. No. 9.3;
RESULT 828
ID ABM73219 standard; protein; 372 AA.
DE Staphylococcus aureus protein #2459.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.2%; Score 86.5; DB 6; Length 372;
Best Local Similarity 18.1%; Pred. No. 1.7;
RESULT 829
ID AAG98347 standard; protein; 396 AA.
DE Escherichia coli protein sequence SEQ ID NO:395.
PN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86; DB 4; Length 396;
Best Local Similarity 21.9%; Pred. No. 1.9;
RESULT 830
ID ABU14798 standard; protein; 396 AA.
DE Protein encoded by prokaryotic essential gene #325.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86; DB 6; Length 396;
Best Local Similarity 21.9%; Pred. No. 1.9;
RESULT 831
ID ABB90798 standard; protein; 725 AA.
DE Herbicidally active polypeptide SEQ ID NO 9.
PN WO200210210-A2.

PD	07-FEB-2002.
PA	(FARR) BAYER AG.
	Query Match 6 .2%; Score 86 ; DB 5 ; Length 725;
	Best Local Similarity 18 .9%; Pred. No. 4 .3 ;
RESULT	832
ID	AB11039 standard; protein; 841 AA.
ID	S. xyloous mpf protein.
PN	DE19914817-A1.
PD	05-OCT-2000.
PA	(PETROR) PETRY GENMEDICS GMBH.
	Query Match 6 .2%; Score 86 ; DB 3 ; Length 841;
	Best Local Similarity 18 .3%; Pred. No. 5 .2 ;
RESULT	833
ID	ABP77912 standard; protein; 295 AA.
ID	N. gonorrhoeae amino acid sequence SEQ ID 2354.
DE	
PN	W200279243-A2.
PD	10-OCT-2002.
PA	(CHIR) CHIRON SPA.
	Query Match 6 .1%; Score 85 .5 ; DB 6 ; Length 295 ;
	Best Local Similarity 21 .6%; Pred. No. 1 .4 ;
RESULT	834
ID	ABU3735 standard; protein; 295 AA.
DE	Protein encoded by Prokaryotic essential gene #22762.
DE	
PW	WO200277103-A2.
PD	03-OCT-2002.
PA	(ELIIT) EULTRA PHARM INC.
	Query Match 6 .1%; Score 85 .5 ; DB 6 ; Length 295 ;
	Best Local Similarity 21 .6%; Pred. No. 1 .4 ;
RESULT	835
ID	ABU39122 standard; protein; 311 AA.
DE	Molecule for disease detection and treatment (MDDT) -32 protein sequence.
PN	WO2003052049-A2.
PD	26-JUN-2003.
PA	(INCYT) INCYTE GENOMICS INC.
	Query Match 6 .1%; Score 85 .5 ; DB 6 ; Length 311 ;
	Best Local Similarity 21 .7%; Pred. No. 1 .5 ;
RESULT	836
ID	ADC37363 standard; protein; 311 AA.
DE	Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 196.
PW	WO2003048202-A2.
PD	12-JUN-2003.
PA	(ASAH) ASAH KASEI KK.
	Query Match 6 .1%; Score 85 .5 ; DB 7 ; Length 311 ;
	Best Local Similarity 21 .7%; Pred. No. 1 .5 ;
RESULT	837
ID	ADR5B59 standard; protein; 311 AA.
DE	Human Elk1 phosphorylation/Elk1 kinase activation protein - SEQ ID 62.
PW	WO2004072277-A2.
PD	26-AUG-2004.
PA	(ASAH) ASAH KASEI PHARMA CORP.
	Query Match 6 .1%; Score 85 .5 ; DB 8 ; Length 311 ;
	Best Local Similarity 21 .7%; Pred. No. 1 .5 ;
RESULT	838
ID	ADU76431 standard; protein; 311 AA.
DE	Progesterone-YOL002c-CGI-45 receptor, INTPO47.
PW	WO2004010161-A2.
PD	25-NOV-2004.
PA	(INPH) INPHARMATICA LTD.
	Query Match 6 .1%; Score 85 .5 ; DB 8 ; Length 311 ;
	Best Local Similarity 21 .7%; Pred. No. 1 .5 ;
RESULT	839
ID	AMM93524 standard; protein; 329 AA.
DE	Human polypeptide, SEQ ID NO: 3257.
PW	EP1130094-A2.
PD	05-SEP-2001.
PA	(HELI) HELIX RES INST.
	Query Match 6 .1%; Score 85 .5 ; DB 4 ; Length 329 ;
	Best Local Similarity 23 .0%; Pred. No. 1 .6 ;
RESULT	840
ID	ABP92687 standard; protein; 329 AA.
DE	Human protein sequence SEQ ID NC:11071.
PW	EP1074017-A2.
PD	07-FEB-2001.

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PA (HELI-1) HELIX RES INST. Query Match 6.1%; Score 85.5; DB 4; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.6;
RESULT 841
ID Adl31224 standard; protein; 329 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3257.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.1%; Score 85.5; DB 8; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.6;
RESULT 842
ID ADA98171 standard; protein; 359 AA.
DE Human secreted protein sequence #12.
PN WO200304623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC. Query Match 6.1%; Score 85.5; DB 6; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 843
ID ADA44024 standard; protein; 359 AA.
DE Human secreted protein SEQ ID 212.
PN WO200300865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC. Query Match 6.1%; Score 85.5; DB 6; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 844
ID ADC20341 standard; protein; 359 AA.
DE Human secreted protein - amino acid sequence #17.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC. Query Match 6.1%; Score 85.5; DB 7; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 845
ID ADF10683 standard; protein; 359 AA.
DE Human secreted protein #5.
PN WO200293085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC. Query Match 6.1%; Score 85.5; DB 7; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 846
ID AAB5546 standard; protein; 360 AA.
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:100.
PN WO20077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE-) ROSEN C A. Query Match 6.1%; Score 85.5; DB 4; Length 360;
Best Local Similarity 23.0%; Pred. No. 1.9;
RESULT 847
ID AAW13171 standard; protein; 439 AA.
DE Non-adrenergic SM binding protein.
PN EPB48059-A1.
PD 17-DEC-1998.
PA (VETI-) VETIGEN. Query Match 6.1%; Score 85.5; DB 2; Length 439;
Best Local Similarity 23.0%; Pred. No. 2.4;
RESULT 848
ID AAB1598 standard; protein; 530 AA.
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:15.
PN WO20077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE-) ROSEN C A. Query Match 6.1%; Score 85.5; DB 4; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.2;
RESULT 849
ID AAY4910 standard; protein; 545 AA.
DE Human secreted protein clone pk36_7 protein sequence SEQ ID NO:1.
PN WO200009552-A1.

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PD 24-FEB-2000.
 PA (GEM) GENETICS INST INC. Score 85.5; DB 3; Length 545;
 Query Match 6.1%; Pred. No. 3.3%;
 Best Local Similarity 23.0%;
 RESULT 850
 ID AAB94667 Standard; protein 545 AA.
 DE Human protein sequence SEQ ID NO:156600.
 FN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI- HELIX RES INST. Score 85.5; DB 4; Length 545;
 Query Match 6.1%; Pred. No. 3.3%;
 Best Local Similarity 23.0%;
 RESULT 851
 ID AAV82460 Standard; protein 579 AA.
 DE Human SN-11044-binding receptor protein SEQ ID NO:4.
 PN WO200014266-A1.
 PD 16-MAR-2000.
 PA (SUMITOMO PHARM CO LTD. Score 85.5; DB 3; Length 579;
 Query Match 6.1%; Pred. No. 3.6%;
 Best Local Similarity 23.0%;
 RESULT 852
 ID AAY82459 Standard; protein 582 AA.
 DE Human SN-11044-binding receptor protein SEQ ID NO:2.
 PN WO200014266-A1.
 PD 16-MAR-2000.
 PA (SUMITOMO PHARM CO LTD. Score 85.5; DB 3; Length 582;
 Query Match 6.1%; Pred. No. 3.6%;
 Best Local Similarity 23.0%;
 RESULT 853
 ID ABB69104 Standard; protein 700 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 34104.
 PN WO20110142-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY. Score 85.5; DB 4; Length 700;
 Query Match 6.1%; Pred. No. 3.6%;
 Best Local Similarity 19.7%;
 RESULT 854
 ID AEB15121 Standard; protein 265 AA.
 DE C glutamicum metabolic pathway regulatory (MR) protein SeqID46.
 PN WO2005153402-A1.
 PD 14-JUL-2005.
 PA (BADI) BASF AG.
 Query Match 6.1%; Score 85; DB 9; Length 265;
 Best Local Similarity 24.1%;
 RESULT 855
 ID ABU34716 Standard; protein 338 AA.
 DE Protein encoded by Prokaryotic essential gene #20313.
 PN WO200217183-A2.
 PD 03-OCT-2002.
 PA (ELIT - ELITRA PHARM INC. Score 85; DB 6; Length 338;
 Query Match 6.1%; Pred. No. 1.9%;
 Best Local Similarity 23.1%;
 RESULT 856
 ID ABU36544 Standard; protein 338 AA.
 DE Protein encoded by Prokaryotic essential gene #22071.
 PN WO200217183-A2.
 PD 03-OCT-2002.
 PA (ELIT - ELITRA PHARM INC. Score 85; DB 6; Length 338;
 Query Match 6.1%; Pred. No. 1.9%;
 Best Local Similarity 23.1%;
 RESULT 857
 ID AAG90802 Standard; protein 419 AA.
 DE C glutamicum protein fragment SEQ ID NO: 4556.
 PN EP1108790-A2.
 PD 20-JUN-2001.
 PA (KIYOWA KOGYO KK. Score 85; DB 4; Length 419;
 Query Match 6.1%; Pred. No. 2.6%;
 Best Local Similarity 24.1%;
 RESULT 858
 ID AAF20418 Standard; protein 419 AA.
 DE Corynebacterium glutamicum CHRS protein.
 PN WO200220572-A2.
 PD 14-MAR-2002.

PA (DEGUS) DEGUSSA AG. Score 85; DB 5; Length 419;
 Query Match 6.1%; Pred. No. 2.6%;
 Best Local Similarity 24.1%;
 RESULT 859
 ID ABB15129 standard; protein 419 AA.
 DE C glutamicum metabolic pathway regulatory (MR) protein SeqID44.
 PN US2005153402-A1.
 PD 14-JUL-2005.
 PA (BADI) BASF AG.
 Query Match 6.1%; Score 85; DB 9; Length 419;
 Best Local Similarity 24.1%; Pred. No. 2.6%;
 RESULT 860
 ID ABB55143 Standard; protein 443 AA.
 DE Lactococcus lactis protein ysFC.
 PN FR2807446-A1.
 PD 12-OCT-2001.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE. Score 85; DB 5; Length 443;
 Query Match 6.1%; Pred. No. 2.8%;
 Best Local Similarity 24.4%;
 RESULT 861
 ID AAU78938 Standard; protein 498 AA.
 DE Mouse Rh type C gene (RHCg) protein.
 PN WO200220719-A2.
 PD 14-MAR-2002.
 PA (NYBL) NEW YORK BLOOD CENT INC. Score 85; DB 5; Length 498;
 Query Match 6.1%; Pred. No. 3.3%;
 Best Local Similarity 20.2%;
 RESULT 862
 ID ADE56674 Standard; protein 1166 AA.
 DE Rat Protein Q03343; SEQ ID NO 2729.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG. Score 85; DB 7; Length 1166;
 Query Match 6.1%; Pred. No. 11;
 Best Local Similarity 19.8%;
 RESULT 863
 ID AAB02010 Standard; protein 1180 AA.
 DE Type VI adenylyl cyclase.
 PN US6107076-A.
 PD 22-AUG-2000.
 PA (TEXA) UNIV TEXAS SYSTEM. Score 85; DB 3; Length 1180;
 Query Match 6.1%; Pred. No. 11;
 Best Local Similarity 19.8%;
 RESULT 864
 ID ADH88320 Standard; protein 286 AA.
 DE Enterococcus faecalis polypeptide #2800.
 PN US6617156-B1.
 PD 09-SEP-2003.
 PA (DOUC /) DOUCETTE-STAMM L A.
 PA (BUSH/) BUSH D.
 Query Match 6.1%; Score 84.5; DB 7; Length 296;
 Best Local Similarity 25.2%;
 RESULT 865
 ID ABM68417 Standard; protein 324 AA.
 DE Photobacterium luminescens protein sequence #1514.
 PN WO200394867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI. Score 84.5; DB 6; Length 324;
 Query Match 6.1%; Pred. No. 2.1%;
 Best Local Similarity 23.8%;
 RESULT 866
 ID AAY0771 Standard; protein 356 AA.
 DE Human secreted protein fragment encoded from gene 28.
 PN WO900155-A1.
 PD 25-FEB-1995.
 PA (HUMA-) HUMAN GENOME SCI INC. Score 84.5; DB 2; Length 356;
 Query Match 6.1%; Pred. No. 2.4%;
 Best Local Similarity 19.8%;
 RESULT 867
 ID ABG75197 Standard; protein 408 AA.
 DE Wheat homogenate geranylgeranyI transferase.

PN WO2003082899-A2.
 PD 09-OCT-2003
 PA (DUPO) DU PONT DE NEMOURS & CO E I .
 Query Match 6.1%; Score 84.5%; DB 7; Length 408;
 Best Local Similarity 25.3%; Pred. No. 2.9;
RESULT 868
 ID AAG46717 standard; protein; 446 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 58803.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 6.1%; Score 84.5%; DB 3; Length 446;
 Best Local Similarity 19.0%; Pred. No. 3.2;
RESULT 869
 ID AAY95015 standard; protein; 453 AA.
 DE Human secreted protein vc6_1, SEQ ID NO:70.
 PN WO200010105-A1.
 PD 02-MAR-2000.
 PA (ALPH-) ALPHAGENE INC.
 Query Match 6.1%; Score 84.5%; DB 3; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 870
 ID AAC65236 standard; protein; 453 AA.
 DE Protein tyrosine kinase 50.
 PN CN1298344-A.
 PD 13-JUN-2001.
 PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
 Query Match 6.1%; Score 84.5%; DB 4; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 871
 ID AAU29065 standard; protein; 453 AA.
 DE Human PRO polypeptide sequence #42.
 PN WO2001616848-A2.
 PD 20-SEP-2001.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 4; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 872
 ID IAM39489 standard; protein; 453 AA.
 DE Human polypeptide SEQ ID NO 2634.
 PN WO200151312-A1.
 PD 26-JUL-2001.
 PA (HYSEQ) HYSEQ INC.
 Query Match 6.1%; Score 84.5%; DB 4; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 873
 ID AAB65170 standard; protein; 453 AA.
 DE Human protein sequence SEQ ID NO:73.
 PN WO20007454-A1.
 PD 07-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 4; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 874
 ID ABB0299 standard; protein; 453 AA.
 DE Human polypeptide SEQ ID NO 2675.
 PN WO200190104-A2.
 PD 29-NOV-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 6.1%; Score 84.5%; DB 5; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 875
 ID ABUS8441 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003027272-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 876
 ID ABUS7989 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003032127-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 877
 ID ABR66178 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003027278-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 878
 ID ABR65568 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003036159-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 879
 ID ABR65568 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003040070-A1.
 PD 27-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 880
 ID ABU99508 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003040070-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 881
 ID ABU57985 standard; protein; 453 AA.
 DE Human PRO polypeptide #17.
 PN US2003027163-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 882
 ID ABU59063 standard; protein; 453 AA.
 DE Novel human secreted or transmembrane protein PRO732.
 PN US2002132252-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 883
 ID ABU82575 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003032033-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 884
 ID ABU82747 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003032113-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 885
 ID ABU89868 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003036147-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 886
 ID ABR68117 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003027264-A1.
 PD 05-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 887

ID ABU60494 standard; protein; 453 AA.
 DB Human secreted/transmembrane protein, #24.
 PN US2002160384-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 888
 ID ABu96170 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003036144-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 889
 ID ABU92601 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003036149-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 890
 ID ABO0678 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US200304923-A1.
 PD 06-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 891
 ID ABO2730 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003040062-A1.
 PD 27-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 892
 ID ABR74884 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003040056-A1.
 PD 27-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 893
 ID ABR94646 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US200304926-A1.
 PD 06-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 894
 ID ABU13876 standard; protein; 453 AA.
 DE Human secreted polypeptide.
 PN US200203125-A1.
 PD 01-AUG-2002.
 PA (GETH) GENENTECH LTD.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 895
 ID ABU85619 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003036140-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 896
 ID ABU98779 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US20030313153-A1.
 PD 16-JAN-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 897

ID ABU97994 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US200301754-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 898
 ID ABU91700 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003027277-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 899
 ID ABU89393 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003036141-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 900
 ID ABU86734 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003036146-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 901
 ID ABU67447 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003036162-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 902
 ID ABU80475 standard; protein; 453 AA.
 DE Human PRO protein #42.
 PN US2003036137-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 903
 ID ABU72461 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003003531-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 904
 ID ABR99393 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003040053-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 905
 ID ABR98783 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003040054-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 906
 ID ABO16106 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003027277-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 907
ID ABR92206 standard; protein; 453 AA. SEQ ID NO: 84.
DE Human secreted polypeptide PRO732, SEQ ID NO: 84.
PN US2003036160-A1.
PD 20-FEB-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 908
ID ABO18847 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044925-A1.
PD 06-MAR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 909
ID ABR78268 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003035474-A1.
PD 20-MAR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036118-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 910
ID ABO15004 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032114-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 911
ID ABO00143 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032101-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 912
ID ABO11475 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42
PN US2003036124-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 913
ID ABO02120 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42
PN US2003040054-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 914
ID ABU88694 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036133-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 915
ID ABO03389 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036134-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 916
ID ABO06190 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022294-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 917
ID ABR59226 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027266-A1.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027275-A1.
PD 06-FEB-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 918
ID ABO0288 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027324-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 919
ID ABO19152 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036118-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036123-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 920
ID ABO1170 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036123-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 921
ID ABR66788 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036148-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 922
ID ABO16001 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003040060-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 923
ID ABO13707 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044916-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 924
ID ABU5510 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036156-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 925
ID ABO07458 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032117-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 926
ID ABO03645 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036128-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;

RESULT 927
ID ABR67093 Standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027266-A1.

PD 06-FEB-2003. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 928
 ID AB015696 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003054483-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 929
 ID ABU55977 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein, PRO732.
 PN US2003222298-A1.
 PD 30-JAN-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 930
 ID ABU65305 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003032102-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 931
 ID ABU95250 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003036117-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 932
 ID ABU71153 standard; protein; 453 AA.
 DE Human PRO732 protein.
 PN US2003036143-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 933
 ID ABO07763 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003032130-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 934
 ID ABR70004 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003032138-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 935
 ID ABR69337 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003036132-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 936
 ID ABC01478 standard; protein; 453 AA.
 DE US20030308353-A1.
 PN 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 937
 ID ABU81280 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003017542-A1.

PD 23-JAN-2003. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 938
 ID ABR60077 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003032137-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 939
 ID ABR67812 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003027269-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 940
 ID ABR65200 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003027258-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 941
 ID ABR68422 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003027274-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 942
 ID ABR71834 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003032135-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 943
 ID ABUS9210 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein, #24.
 PN US2003027152-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 944
 ID ABUS5314 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003022295-A1.
 PD 30-JAN-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 945
 ID ABUS9004 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003022297-A1.
 PD 30-JAN-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 946
 ID ABU83084 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003032105-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 947
 ID ABU94940 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003032123-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 948
 ID ABU8399 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003032108-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 949
 ID ABU8399 standard; protein; 453 AA.
 DE Novel secreted/transmembrane protein (PRO) #42.
 PN US2003032111-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 950
 ID ABU83650 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003032119-A1.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 951
 ID ABO5907 standard; protein; 453 AA.
 DE Human secreted polypeptide.
 PN US2002127576-A1.
 PD 12-SEP-2002.
 PA (GPTH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 952
 ID ABR64895 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US20030307263-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 953
 ID ABR68727 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US200303027271-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 954
 ID ABO16543 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US20030316125-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 955
 ID ABR99088 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003040168-A1.
 PD 27-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 956
 ID ABR6972 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US20030327280-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 957
 ID ABR85924 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US20030322300-A1.
 PD 30-JAN-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 958
 ID ABUB211 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003036136-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 959
 ID ABUB222 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003036138-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 960
 ID ABUB3694 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003032109-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 961
 ID ABO08068 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003040066-A1.
 PD 27-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 962
 ID ABUB1779 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003032104-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 963
 ID ABU65943 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003036157-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 964
 ID ABR59772 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003032120-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 965
 ID ABU99360 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003036155-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 966
 ID ABU99813 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US20030322296-A1.
 PD 30-JAN-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 967
 ID ABR66483 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US20030327281-A1.
 PD 06-FEB-2003.
 PA (GPTH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 968
 ID ABR90901 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 FN 003-04055-A1.
 PD 27-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 969
 ID ABU58916 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein, #24.
 PN US20030142951-A1.
 PD 03-OCT-2002.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5%; DB 6; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3;
 ID ABU94128 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003017540-A1.
 PD 23-JAN-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 970
 ID ABU79210 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003032106-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 ID ABU65339 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003032129-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 972
 ID ABU86444 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003032131-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 ID ABU94633 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003032103-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 974
 ID ABU94633 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003032103-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 975
 ID ABO04560 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003032107-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 ID ABR70109 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003032139-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 977
 ID ABU92294 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003022187-A1.
 PD 30-JAN-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 978
 ID ABU98474 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003022301-A1.

PD 30-JAN-2003.
 Query Match Best Local Similarity 6.1%; Score 84.5%; DB 6; Length 453;
 RESULT 979
 ID ABR65873 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003036165-A1.
 PD 20-FBB-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5%; DB 6; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 980
 ID ABR64590 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003027462-A1.
 PD 06-FBB-2003.
 Query Match Best Local Similarity 6.1%; Score 84.5%; DB 6; Length 453;
 RESULT 981
 ID ABUS3359 standard; protein; 453 AA.
 DE Novel human secreted or transmembrane protein PRO1120.
 PN US2003027985-A1.
 PD 06-FBB-2003.
 Query Match Best Local Similarity 6.1%; Score 84.5%; DB 6; Length 453;
 RESULT 982
 ID ABUT8515 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003032110-A1.
 PD 13-FBB-2003.
 Query Match Best Local Similarity 6.1%; Score 84.5%; DB 6; Length 453;
 RESULT 983
 ID ABU92906 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003036142-A1.
 PD 20-FBB-2003.
 Query Match Best Local Similarity 6.1%; Score 84.5%; DB 6; Length 453;
 RESULT 984
 ID ABU93865 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003036145-A1.
 PD 20-FBB-2003.
 Query Match Best Local Similarity 6.1%; Score 84.5%; DB 6; Length 453;
 RESULT 985
 ID ABU91085 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003036153-A1.
 PD 20-FBB-2003.
 Query Match Best Local Similarity 6.1%; Score 84.5%; DB 6; Length 453;
 RESULT 986
 ID ABU90178 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003044931-A1.
 PD 06-MAR-2003.
 Query Match Best Local Similarity 6.1%; Score 84.5%; DB 6; Length 453;
 RESULT 987
 ID ABO09593 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003036153-A1.
 PD 20-FBB-2003.
 Query Match Best Local Similarity 6.1%; Score 84.5%; DB 6; Length 453;
 RESULT 988
 ID ABO10865 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003036150-A1.
 PD 20-FBB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 989
ID ABR9119 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040059-A1.
PD 27-FEB-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 990
ID ABU87527 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032293-A1.
PD 30-JAN-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 991
ID ABU91395 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032128-A1.
PD 13-FEB-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 992
ID ABU84609 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032116-A1.
PD 13-FEB-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 993
ID ABK9699 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032122-A1.
PD 13-FEB-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 994
ID ABU0076 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036139-A1.
PD 20-FEB-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 995
ID ABU92125 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017476-A1.
PD 23-JAN-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 996
ID ABU93345 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003017541-A1.
PD 23-JAN-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 997
ID AB009898 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003017543-A1.
PD 23-JAN-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 998
ID AB008983 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US20030186152-A1.
PD 20-FEB-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 999
ID ABU10831 standard; protein; 453 AA.

DE Human PRO polypeptide #17.
PN US2002123463-A1.
PD 05-SEP-2002.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1000
ID ABU10551 standard; protein; 453 AA.
DE Human secreted/transmembrane protein #42.
PN US2001127584-A1.
PD 12-SEP-2002.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1001
ID ABU81583 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002177164-A1.
PD 28-NOV-2002.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1002
ID ABU95560 standard; protein; 453 AA.
DE Human PRO Polypeptide #42.
PN US2003032115-A1.
PD 13-FEB-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1003
ID ABU95669 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032140-A1.
PD 13-FEB-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1004
ID ABR0514 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040076-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1005
ID ABO04165 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003008357-A1.
PD 09-JAN-2003.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1006
ID ABO08373 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044922-A1.
PD 06-MAR-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1007
ID ABU88522 standard; protein; 453 AA.
DE Human secreted and transmembrane polypeptide PRO732.
PN US2002197615-A1.
PD 26-DEC-2002.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5%; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1008
ID AB034056 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
 ID ABR0550 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003032118-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1010
 ID ABR73989 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003036135-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1011
 ID ABR05511 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054455-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1012
 ID ABR80858 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049741-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1013
 ID ABR81163 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049743-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1014
 ID ABR08859 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049769-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1015
 ID ABR88461 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054479-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1016
 ID ABR7282 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054479-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1017
 ID ABO28766 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003058685-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1018
 ID ABO31511 standard; protein; 453 AA.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1028
 ID ABR94951 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003073183-A1.
 PD 06-MAR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1029
 ID ABR95256 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003044930-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1030
 ID ABO21494 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003054471-A1.

PD 20-MAR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1031
 ID ABR97758 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003064452-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1032
 ID ABR97546 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068705-A1.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1033
 ID ABM77587 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054473-A1.

PD 20-MAR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1034
 ID ABM27817 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003064440-A1.

PD 03-APR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1035
 ID ABM06098 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US20030656704-A1.

PD 10-APR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1036
 ID ABM03604 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003058722-A1.

PD 10-APR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1037
 ID ABO27546 standard; protein; 453 AA.

ID ABM35055 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003073183-A1.
 PD 17-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1038
 ID ABM26292 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003104549-A1.

PD 05-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1039
 ID ABO48074 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US200309749-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1040
 ID ABR92816 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003064462-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1041
 ID ABO24577 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003065159-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1042
 ID ADA37384 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.

PN US2003008297-A1.

PD 09-JAN-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1043
 ID ABM1188 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003064447-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1044
 ID ABM02659 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003073184-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1045
 ID ABM15985 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003064465-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1046
 ID ABO27546 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.
 PN US200310451-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3; SEQ ID NO:84.
RESULT 1047
 ID ABM2007 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 DE Human secreted polypeptide PRO732-A1.
 PN US2003068721-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3; SEQ ID NO:84.
RESULT 1048
 ID ABM7013 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068699-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3; SEQ ID NO:84.
RESULT 1049
 ID ABM2107 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068707-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3; SEQ ID NO:84.
RESULT 1050
 ID ABM0453 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003073175-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3; SEQ ID NO:84.
RESULT 1051
 ID ABO41323 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068695-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3; SEQ ID NO:84.
RESULT 1052
 ID ABO36138 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003068703-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3; SEQ ID NO:84.
RESULT 1053
 ID ABO43667 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003068732-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3; SEQ ID NO:84.
RESULT 1054
 ID ABM76367 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003082717-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3; SEQ ID NO:84.
RESULT 1055
 ID ABM76063 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003104548-A1.

PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
RESULT 1056
 ID ABM25682 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003104542-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
RESULT 1057
 ID ABM25987 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003104543-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
RESULT 1058
 ID ADA21270 standard; protein; 453 AA.
 DE Human secreted/transmembrane polypeptide PRO732.
 PN US2003054404-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
RESULT 1059
 ID ABO0340 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003054412-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
RESULT 1060
 ID ABO02425 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US20030404061-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
RESULT 1061
 ID ABR90596 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003036130-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
RESULT 1062
 ID ABR73664 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054468-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
RESULT 1063
 ID ABO16216 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003054470-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
RESULT 1064
 ID ABR4341 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003044917-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
RESULT 1065
 ID ABR75948 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003044929-A1.

PD 06-MAR-2003. Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1066 ID ABM0843 standard; protein; 453 AA.
 ID ABR71224 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003059880-A1.
 PD 27-MAR-2003 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1067 ID ABR93121 standard; protein; 453 AA.
 ID ABR93121 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003059885-A1.
 PD 03-APR-2003 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1068 ID ABR93426 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003059465-A1.
 PD 20-MAR-2003 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1069 ID ABR10057 standard; protein; 453 AA.
 ID ABR10057 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein, PRO732.
 PN US2003054478-A1.
 PD 27-MAR-2003 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1070 ID ABR87851 standard; protein; 453 AA.
 ID ABR87851 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003059831-A1.
 PD 10-APR-2003 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1071 ID ABO111893 standard; protein; 453 AA.
 ID ABO111893 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US200304555-A1.
 PD 03-APR-2003 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1072 ID ABO299886 standard; protein; 453 AA.
 ID ABO299886 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US20030564461-A1.
 PD 03-APR-2003 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1073 ID ABO31195 standard; protein; 453 AA.
 ID ABO31195 standard; protein; 453 AA.
 DE Human secreted polypeptide #42.
 PN US20030568724-A1.
 PD 10-APR-2003 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1074 ID ABM04883 standard; protein; 453 AA.
 ID ABM04883 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US20030568727-A1.
 PD 10-APR-2003 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
 Query Match 6.1%; Score 84.5; DB 6; Length 453;

ID ADA17601 standard; protein; 453 AA.	PN US2003068740-A1.
DB Human secreted polypeptide.	PD 10-APR-2003.
PN US2003054987-A1.	PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 6; Length 453;
PD 20-MAR-2003.	Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;	RESULT 1085
ID ABR7148 standard; protein; 453 AA.	DB ABM07623 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054481-A1.	PN US2003068751-A1.
PD 20-MAR-2003.	PD 10-APR-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;	Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;	RESULT 1086
ID ABR86936 standard; protein; 453 AA.	DB ABO40713 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049778-A1.	PN US2003068884-A1.
PD 13-MAR-2003.	PD 10-APR-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;	Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;	RESULT 1087
ID ABM10978 standard; protein; 453 AA.	DB ABM35360 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049782-A1.	PN US2003073179-A1.
PD 13-MAR-2003.	PD 17-APR-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;	Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;	RESULT 1088
ID ABM2122 standard; protein; 453 AA.	DB ABM33123 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054476-A1.	PN US2003087374-A1.
PD 20-MAR-2003.	PD 08-MAY-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;	Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;	RESULT 1089
ID ABO32121 standard; protein; 453 AA.	DB ABO5249 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.	DE Human PRO polypeptide #42.
PN US2003068733-A1.	PN US2003049773-A1.
PD 10-APR-2003.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;	Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;	RESULT 1090
ID ABM15248 standard; protein; 453 AA.	DB ABO50109 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068692-A1.	PN US2003049777-A1.
PD 10-APR-2003.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;	Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;	RESULT 1091
ID AEM06403 standard; protein; 453 AA.	DB ABU99203 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068709-A1.	PN US2003040055-A1.
PD 10-APR-2003.	PD 27-FEB-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;	Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;	RESULT 1092
ID AEM04214 standard; protein; 453 AA.	DB ABO5685 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068716-A1.	PN US2003040074-A1.
PD 10-APR-2003.	PD 27-FEB-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;	Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3..3;	RESULT 1093
ID ABM22327 standard; protein; 453 AA.	DB ABO5685 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	DE Human secreted/transmembrane protein (PRO) #42.

RESULT 1103
 ID ABM18425 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054480-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1104
 ID ADA27709 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003054359-A1.
 PD 20-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1105
 ID ABR97453 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003059885-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1106
 ID ABM80553 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049740-A1.
 PD 15-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1107
 ID ABM01164 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049770-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1108
 ID ABM88766 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003072169-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1109
 ID ABM13418 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003064547-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1110
 ID ABM20802 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003058871-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1111
 ID ABC19333 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003049745-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1112
 ID ABO12543 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.

RESULT 1122
 ID ABM6631 standard; protein; 453 AA. SEQ ID NO:84.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049772-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1123
 ID ABM16595 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US200304448-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1124
 ID ABM29647 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US200306456-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1125
 ID ABO29071 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068693-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1126
 ID ABM23852 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068735-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1127
 ID ABM23212 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068753-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1128
 ID ABM22022 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068742-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1129
 ID AB03763 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068756-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1130
 ID ABM28427 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US20030822715-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1131
 ID ABM28732 standard; protein; 453 AA.

Best Local Similarity	19.8%	Pred. No.	3.3;
RESULT 1141			
ID ABR85716 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US2013049753-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1142			
ID ABR93698 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US2013049763-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1143			
ID ABM0554 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US2013073172-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1144			
ID ABM00249 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US2013073172-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1145			
ID ABO29581 standard; protein; 453 AA.			
DE Human secreted/transmembrane protein (PRO) #42.			
PN US2013068700-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1146			
ID ABR23547 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US2013068736-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1147			
ID ABR29142 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US2013068679-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1148			
ID ABO38273 standard; protein; 453 AA.			
DE Human secreted/transmembrane protein (PRO) #42.			
PN US2013068767-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1149			
ID ABO45573 standard; protein; 453 AA.			
DE Human secreted polypeptide #42.			
PN US2013073182-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1150			
ID ABM20497 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US2013073171-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1151			
ID ADB1355 standard; protein; 453 AA.			
DE Human secreted/transmembrane protein (PRO) #42.			
PN US2013092121-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1152			
ID ABO16611 standard; protein; 453 AA.			
DE Human secreted/transmembrane protein (PRO) #42.			
PN US2013021226-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1153			
ID ABO18237 standard; protein; 453 AA.			
DE Human secreted/transmembrane protein (PRO) #42.			
PN US20130494920-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1154			
ID ABO22664 standard; protein; 453 AA.			
DE Human PRO polypeptide #42.			
PN US2013022265-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1155			
ID ABO22969 standard; protein; 453 AA.			
DE Human PRO polypeptide #42.			
PN US2013054461-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1156			
ID ABR9511 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US2013064446-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1157			
ID ABR81468 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US201304974-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1158			
ID ABM77892 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US2013049783-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			
RESULT 1159			
ID ABR89581 standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.			
PN US2013073171-A1.			
PA (GETH) GENENTECH INC.			
Query Match 6.1%; Score 84.5; DB 6; Length 453;			
Best Local Similarity 19.8%; Pred. No. 3.3;			

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1160 Human secreted polypeptide PRO732, SEQ ID NO:84.

ID ABM25072 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US200310450-A1.

PD 05-JUN-2003.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1161 Human secreted polypeptide PRO732, SEQ ID NO:84.

ID ABM13723 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003064458-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1162 Ab028461 standard; protein; 453 AA.

ID ABO30909 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.

PN US2003064456-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1163 ABO30291 standard; protein; 453 AA.

ID ABO30291 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.

PN US2003064464-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1164 ABM07318 standard; protein; 453 AA.

ID ABO303909 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003068702-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1165 ABM07318 standard; protein; 453 AA.

ID ABO303909 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003068734-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1166 ABO307053 standard; protein; 453 AA.

ID ABO307053 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.

PN US2003068719-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1167 ABM1638 standard; protein; 453 AA.

ID ABO41638 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.

PN US2003068729-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1168 ABO35223 standard; protein; 453 AA.

ID ABO35223 standard; protein; 453 AA.

DE Human PRO polypeptide #42.

PN US2003068738-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1169 Human secreted polypeptide PRO732, SEQ ID NO:84.

ID ABM16300 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003040078-A1.

PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1170 ABO47464 standard; protein; 453 AA.

ID ABO47464 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.

PN US2003049742-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1171 ABO147769 standard; protein; 453 AA.

ID ABO147769 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.

PN US2003049747-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1172 ABO48379 standard; protein; 453 AA.

ID ABO48379 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.

PN US2003049750-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1173 ABO51129 standard; protein; 453 AA.

ID ABO51129 standard; protein; 453 AA.

DE Human PRO polypeptide #42.

PN US2003049756-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1174 ABO51734 standard; protein; 453 AA.

ID ABO51734 standard; protein; 453 AA.

DE Human PRO polypeptide #42.

PN US2003049767-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1175 ABO50514 standard; protein; 453 AA.

ID ABO50514 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.

PN US2003049779-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1176 ABR79638 standard; protein; 453 AA.

ID ABR79638 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.

PN US2003040059-A1.

PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1177 ABM16900 standard; protein; 453 AA.

ID ABM16900 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003040078-A1.

PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5%; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1178 ABO17332 standard; protein; 453 AA.

ID ABO17332 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.

PN US200304918-A1.

PD 06-MAR-2003. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1179 ID ABO20894 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US20030313213-A1.
PD 13-FEB-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1180 ID ABR96843 standard; protein; 453 AA. SEQ ID NO:84.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054462-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1181 ID ADA38514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059780-A1.
PD 27-MAR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1182 ID AM12198 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064445-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1183 ID ABM16290 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064449-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1184 ID ABM14157 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064441-A1.
PD 03-APR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1185 ID ABM14638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003058696-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1186 ID ABM04519 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US20030586712-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1187 ID ABM06708 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003058730-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1188 ID ABM09148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073174-A1.
PD 17-APR-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1189 ID ABO39188 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068775-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1190 ID ABM73453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104545-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1191 ID ABM25377 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104541-A1.
PD 05-JUN-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1192 ID ABM19887 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104554-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1193 ID ABO46793 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049762-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1194 ID ABO47098 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049765-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1195 ID ADA83153 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049752-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1196 ID ABR71529 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032133-A1.
PD 13-FEB-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1197 ID ABR72139 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032136-A1.
PD 13-FEB-2003.

Query Match	6.1%	Score 84.5; DB 6;	Length 453;	
Best Local Similarity	19.8%	Pred. No. 3..3;		
RESULT 1198				
ID ABR98478	standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
PN US2003036129-A1.				
PD 20-FEB-2003.				
Query Match	6.1%	Score 84.5; DB 6;	Length 453;	
Best Local Similarity	19.8%	Pred. No. 3..3;		
RESULT 1199				
ID ABO68418	standard; protein; 453 AA.			
DE Human secreted/transmembrane protein (PRO) #42.				
PN US2003040053-A1.				
PD 27-FEB-2003.				
Query Match	6.1%	Score 84.5; DB 6;	Length 453;	
Best Local Similarity	19.8%	Pred. No. 3..3;		
RESULT 1200				
ID ABR84801	standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
PN US2003040057-A1.				
PD 27-FEB-2003.				
Query Match	6.1%	Score 84.5; DB 6;	Length 453;	
Best Local Similarity	19.8%	Pred. No. 3..3;		
RESULT 1201				
ID ABR73359	standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
PN US2003054467-A1.				
PD 20-MAR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	6.1%	Score 84.5; DB 6;	Length 453;	
Best Local Similarity	19.8%	Pred. No. 3..3;		
RESULT 1202				
ID ABR76453	standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
PN US2003044932-A1.				
PD 06-MAR-2003.				
Query Match	6.1%	Score 84.5; DB 6;	Length 453;	
Best Local Similarity	19.8%	Pred. No. 3..3;		
RESULT 1203				
ID ABR73054	standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
PN US2003042720-A1.				
PD 06-FEB-2003.				
Query Match	6.1%	Score 84.5; DB 6;	Length 453;	
Best Local Similarity	19.8%	Pred. No. 3..3;		
RESULT 1204				
ID ABM18120	standard; protein; 453 AA.			
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
PN US2003054469-A1.				
PD 20-MAR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	6.1%	Score 84.5; DB 6;	Length 453;	
Best Local Similarity	19.8%	Pred. No. 3..3;		
RESULT 1205				
ID ABO20579	standard; protein; 453 AA.			
DE Human secreted/transmembrane protein (PRO) #42.				
PN US2003032126-A1.				
PD 13-FEB-2003.				
Query Match	6.1%	Score 84.5; DB 6;	Length 453;	
Best Local Similarity	19.8%	Pred. No. 3..3;		
RESULT 1206				
ID ABO25322	standard; protein; 453 AA.			
DE Human PRO polypeptide #42.				
PN US2003054467-A1.				
PD 20-MAR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	6.1%	Score 84.5; DB 6;	Length 453;	
Best Local Similarity	19.8%	Pred. No. 3..3;		
RESULT 1207				
ID ABO25657	standard; protein; 453 AA.			
DE Human PRO polypeptide #42.				
PN US2003054466-A1.				
PD 20-MAR-2003.				

RESULT 1217
ID ABM5488 standard; protein; 453 AA. SEQ ID NO:84.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1218
ID ABM1553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068690-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1219
ID ABM0538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1220
ID AB042218 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003149748-A1.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1221
ID AB037968 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1222
ID AB045878 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1223
ID ABM6681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068688-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1224
ID ADB20196 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US200310452767-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1225
ID ABM19582 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104552-A1.
PD 01-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1226
ID AB049294 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003036126-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1236 ABR74579 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID US200304924-A1.
 PN 06-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1237 ABR77058 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID US200304927-A1.
 PN 06-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1238 ABM17815 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID US2003040072-A1.
 PN 27-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1239 ABM95866 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID US2003054475-A1.
 PN 27-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1240 ABO21799 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003054475-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1241 ABO19969 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003032124-A1.
 PD 13-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1242 ABO42472 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US20030364467-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1243 ABR86021 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID US2003049759-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1244 ABR10673 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID US2003064455-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1245 AM76672 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 ID US2003049757-A1.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054465-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1246 ABR89376 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID US2003073170-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1247 ABM12503 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID ABM05793 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID ABM05793 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID ABM34918 standard; protein; 453 AA.
 DE Human secreted polypeptide #42.
 PN US2003068717-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1248 ABO21799 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID ABM02994 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID ABM18972 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID ABM19277 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID ABM19277 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 ID ABM46188 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003049761-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1253 ABO42472 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 ID ABO42472 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 ID ABO42472 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 ID ABO42472 standard; protein; 453 AA.

PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1255
 ID ABR89012 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003027223-A1.
 PD 06-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1256
 ID ABR89011 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003027223-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1257
 ID ABR7444 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003036120-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1258
 ID ABR74274 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003036161-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1259
 ID ABR18542 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US200304921-A1.
 PD 06-MAR-2003.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1260
 ID ABR80248 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049739-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1261
 ID ABR01469 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003059882-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1262
 ID ABR02079 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003059884-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1263
 ID ABR87241 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003059887-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1264
 ID ABR01124 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.

ID ABM12808 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003073196-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1265
 ID ABM30562 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003064443-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1266
 ID ABM24462 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003064444-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1267
 ID ABO29376 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068637-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1268
 ID ABO31206 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068710-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1269
 ID ABO1433 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068636-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1270
 ID ABO09758 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068635-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1271
 ID ABO38863 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068774-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1272
 ID ABM34648 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003104538-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3%;
 RESULT 1273
 ID ABO1124 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.

PN US2003049781-A1.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1274
 ID ABO03950 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003036158-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1275
 ID ABO10420 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003036151-A1.
 PD 20-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1276
 ID ABO53122 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003044806-A1.
 PD 05-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1277
 ID ABR77663 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003040067-A1.
 PD 27-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1278
 ID ABR77873 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054456-A1.
 PD 20-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1279
 ID ABO23967 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003054482-A1.
 PD 20-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1280
 ID ABR93711 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054457-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1281
 ID ABO1174 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003059883-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1282
 ID ABM78197 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049764-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1283
 ID ABR89986 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003073177-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1284
 ID ADA22196 standard; protein; 453 AA.
 DE Human secreted/transmembrane polypeptide PRO732.
 PN US2003040473-A1.
 PD 27-FEB-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1285
 ID ABM27512 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003064442-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1286
 ID ABM13113 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003064450-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1287
 ID ABO31816 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068731-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1288
 ID ABM14028 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068663-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1289
 ID ABM08933 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068754-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1290
 ID ABM08934 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068661-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1291
 ID ABM74338 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003096351-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3..3;
 RESULT 1292
 ID ABM33733 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003096358-A1.
 PD 22-MAY-2003.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3; Length 453;
 RESULT 1293 ID ABR20192 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732; SEQ ID NO:84.
 PN US2003104556-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3; Length 453;
 RESULT 1294 ID ABO48614 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003049756-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3; Length 453;
 RESULT 1295 ID ABO22492 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US200317982-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3; Length 453;
 RESULT 1296 ID ABR72749 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732; SEQ ID NO:84.
 PN US2003036122-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3; Length 453;
 RESULT 1297 ID ABO15391 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003036121-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3; Length 453;
 RESULT 1298 ID ABR88106 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732; SEQ ID NO:84.
 PN US2003040065-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3; Length 453;
 RESULT 1299 ID ABO15086 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003044919-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3; Length 453;
 RESULT 1300 ID ABO17221 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003040077-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3; Length 453;
 RESULT 1301 ID ABH17510 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732; SEQ ID NO:84.
 PN US200304928-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Query Match Best Local Similarity 19.8%; Pred. No. 3.3; Length 453;
 RESULT 1302 ID ADA06362 standard; protein; 453 AA.
 DE Human secreted/transmembrane PRO polypeptide #17.
 PN US2003049638-A1.

Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1312 ID AB041018 standard; protein: 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US0030368694-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1313 ID AB036748 standard; protein: 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US20030368715-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1314 ID AB037358 standard; protein: 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US20030368726-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1315 ID ABM75148 standard; protein: 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US200304544-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1316 ID ABM33428 standard; protein: 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003096357-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1317 ID AB046103 standard; protein: 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003149760-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1318 ID ADA82519 standard; protein: 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US20030349755-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1319 ID ADB96081 standard; protein: 453 AA.
 DE Human PRO polypeptide #17.
 PN US2003054403-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1320 ID ABM31782 standard; protein: 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US20030686680-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1321 ID ABM31172 standard; protein: 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003044315-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5%; DB 7; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1331
 ID ADC1261 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003068637-A1.
 PD 10-APR-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1332
 ID ADC1261 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003069403-A1.
 PD 10-APR-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1333
 ID ADC14373 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003082546-A1.
 PD 01-MAY-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1334
 ID ADD07905 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003068623-A1.
 PD 10-APR-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1335
 ID ADC81730 standard; protein; 453 AA.
 DE Human PRO polypeptide #17.
 PN US2003083461-A1.
 PD 01-MAY-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1336
 ID ADD07372 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2002193299-A1.
 PD 19-DEC-2002.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1337
 ID ADC77580 standard; protein; 453 AA.
 DE Human RMS2 amino acid sequence.
 PN WO2003066829-A2.
 PD 14-AUG-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1338
 ID ADC82263 standard; protein; 453 AA.
 DE Human PRO polypeptide #17.
 PN US2003050833-A1.
 PD 27-MAR-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1339
 ID ADD05557 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US200308376-A1.
 PD 08-MAY-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1340
 ID ADD08443 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003073090-A1.
 PD 17-APR-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1341
 ID ADD06692 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2002193300-A1.
 PD 19-DEC-2002.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1342
 ID ADCB8939 standard; protein; 453 AA.
 DE Human PRO polypeptide #17.
 PN US2003059783-A1.
 PD 27-MAR-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1343
 ID ADD55046 standard; protein; 453 AA.
 DE Human PRO polypeptide #17.
 PN US2003077593-A1.
 PD 24-APR-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1344
 ID ADD55004 standard; protein; 453 AA.
 DE Human PRO polypeptide #17.
 PN US2003077594-A1.
 PD 24-APR-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1345
 ID ADD54442 standard; protein; 453 AA.
 DE Human PRO polypeptide #17.
 PN US2002132253-A1.
 PD 19-SEP-2002.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1346
 ID ADE26596 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003087304-A1.
 PD 08-MAY-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1347
 ID ADE26663 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003087305-A1.
 PD 08-MAY-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1348
 ID ADF67000 standard; protein; 453 AA.
 DE Human PRO732 amino acid sequence SEQ ID NO:73.
 PN US2002198148-A1.
 PD 26-DEC-2002.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1349
 ID ADG02552 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003207397-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1350
 ID ADG0255 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003207399-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3; Pred. No. 3 .3;

RESULT 1351
 ID ADG95414 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003207398-A1.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1352
 ID ADG12249 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003207392-A1.

PD 06-NOV-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1353
 ID ADH8909 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003207395-A1.

PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

PD 13-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1354
 ID ADI35254 standard; protein; 453 AA.
 DE Human PRO polypeptide #17.
 PN US2003050457-A1.

PD 13-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1355
 ID ADH97416 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003049682-A1.

PD 13-MAR-2003.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1356
 ID ADL32630 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003207396-A1.

PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1357
 ID ADM30224 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003073813-A1.

PD 17-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1358
 ID ADB74221 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003211572-A1.

PD 13-NOV-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1359
 ID ADB74833 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003211574-A1.

PD 13-NOV-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1360
 ID ADF35199 standard; protein; 453 AA.
 DE Human PRO732 polypeptide.

PN US2003194760-A1.
 PD 16-OCT-2003.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;
 RESULT 1361
 ID ADG11449 standard; protein; 453 AA.
 DE Human PRO732 polypeptide.
 PN US2003228655-A1.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1362
 ID ADP96446 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003215909-A1.

PD 20-NOV-2003.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;
 RESULT 1363
 ID ADG04317 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003215912-A1.

PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1364
 ID ADG00477 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003215911-A1.

PD 20-NOV-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1365
 ID ADG82733 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003215910-A1.

PD 20-NOV-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1366
 ID ADH26114 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003068770-A1.

PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1367
 ID ADH19319 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003228656-A1.

PD 11-DEC-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1368
 ID ADH32883 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003068768-A1.

PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1369
 ID ADH32883 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003224358-A1.

PD 04-DEC-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3 .3;

RESULT 1370
 ID ADH20812 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003224358-A1.

PD 04-DEC-2003.
 PA (GETH) GENENTECH INC. 6.1%; Score 84.5; DB 8; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1370 ID ADH19852 Standard; protein; 453 AA.
 ID Human secreted/transmembrane protein PRO732.
 DE US2003219856-A1.
 PN PD 27-NOV-2003.
 PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1371 ID ADJ54722 Standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US20042123321-A1.
 PD 05-FEB-2004.
 PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1372 ID Adu64433 Standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2004318337-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1373 ID ADM31399 Standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US200448334-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1374 ID ADM36436 Standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US200453358-A1.
 PD 18-MAR-2004.
 PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1375 ID ADM40241 Standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2004048335-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1376 ID EP1447413-A1. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 DE Novel human secreted and transmembrane protein PRO732.
 PN 13-MAY-2004.
 PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1377 ID ADR019184 Standard; protein; 453 AA.
 DE Human protein useful for treating neurological disease Seq 2690.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS - RES ASSOC BIOTECHNOLOGY Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1378 ID ABN0816 Standard; protein; 453 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO81457, SEQ:2102.
 PN WO2004303615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1379 ID AD99176 Standard; protein; 453 AA.
 DE KIAA1253, SEQ ID 182.
 PN WO2004078035-A2.
 PD 16-SEP-2004.
 PA (FARB) BAYER PHARM CORP. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1380 ID ADG6528 Standard; protein; 453 AA.
 DE Human tyrosine kinase 50 amino acid sequence - SEQ ID 2.
 PN CN1510134-A.
 PD 07-JUL-2004.
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI. Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1381 ID AEA38376 Standard; protein; 453 AA.
 DE Human secreted/transmembrane protein cDNA, #86.
 PN US200512725-A1.
 PD 26-MAY-2005.
 PA (GETH) GENENTECH INC. Query Match 6.1%; Score 84.5; DB 9; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1382 ID AED50079 Standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2005163766-A1.
 PD 28-JUL-2005.
 Query Match 6.1%; Score 84.5; DB 9; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.3;
 RESULT 1383 ID ADG1018 Standard; protein; 472 AA.
 DE Human STAT6-activating protein, SEQ ID NO:208.
 PN WO200596943-A1.
 PD 05-DEC-2002.
 PA (ASAHI) ASAHI KASEI KOGYO KK. Query Match 6.1%; Score 84.5; DB 7; Length 472;
 Best Local Similarity 19.8%; Pred. No. 3.5;
 RESULT 1384 ID AAM41275 Standard; protein; 477 AA.
 DE Human polypeptide SEQ ID NO 6206.
 PN WO2001533312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSQ INC. Query Match 6.1%; Score 84.5; DB 4; Length 477;
 Best Local Similarity 19.8%; Pred. No. 3.6;
 RESULT 1385 ID AAG46716 Standard; protein; 521 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 58802.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 6.1%; Score 84.5; DB 3; Length 521;
 Best Local Similarity 19.8%; Pred. No. 4;
 RESULT 1386 ID ABB93183 Standard; protein; 562 AA.
 DE Herbicidally active polypeptide SEQ ID NO 2994.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG. Query Match 6.1%; Score 84.5; DB 5; Length 562;
 Best Local Similarity 19.6%; Pred. No. 4.5;
 RESULT 1387 ID AG46715 Standard; protein; 571 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 58801.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 6.1%; Score 84.5; DB 3; Length 571;
 Best Local Similarity 19.8%; Pred. No. 4.5;
 RESULT 1388 ID ADX95745 Standard; protein; 600 AA.
 DE Plant full length insert polypeptide seqid 58409.
 PN US2004034888-A1.

PD	19-FEB-2004.		PN	US6610836-B1.
PA	(LIUJ/)	LIU J.	PD	26-AUG-2003.
PA	(ZHOU/)	ZHOU Y.	PA	(GENO-) GENOME THERAPEUTICS CORP.
PA	(KOVALIC D K.		Query Match	6.0%;
PA	(SCRE/)	SCREEN S E.	Best Local Similarity	18.1%;
PA	(TABA/)	TABASKA J E.	Pred. No.	4.8;
PA	(CAOY/)	CAO Y.	ID	ABU38257 standard; protein; 575 AA.
PA	Query Match	6.1%;	DE	Protein encoded by Prokaryotic essential gene #23784.
PA	Best Local Similarity	23.0%;	DN	WO200277183-A2.
RESULT	1389		PD	03-OCT-2002.
ID	ADA36714	standard; protein; 241 AA.	PA	(ELIT-) ELITRA PHARM INC.
DE	Acinetobacter baumannii	protein #3875.	Query Match	6.0%;
PN	US6562558-B1.		Best Local Similarity	20.3%;
PD	13-MAY-2003.		Pred. No.	5.2;
PA	(GENO-) GENOME THERAPEUTICS CORP.		RESULT	1398
PA	Query Match	6.0%;	ID	ABO73781 standard; protein; 602 AA.
PA	Best Local Similarity	22.8%;	DE	Pseudomonas aeruginosa polypeptide #5956.
RESULT	1390		PN	US6551795-B1.
ID	ABG61495	standard; protein; 318 AA.	PD	22-APR-2003.
DE	Iron uptake ABC transporter	polypeptide #2.	PA	(GENO-) GENOME THERAPEUTICS CORP.
PN	WO20024773-A2.		Query Match	6.0%;
PD	02-MAY-2002.		Best Local Similarity	20.3%;
PA	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.		Pred. No.	5.6;
PA	Query Match	6.0%;	ID	ABO70835 standard; protein; 720 AA.
PA	Best Local Similarity	24.4%;	DE	Pseudomonas aeruginosa polypeptide #3010.
RESULT	1391		PN	US6551795-B1.
ID	ABU02362	standard; protein; 318 AA.	PD	22-APR-2003.
DE	S. pneumoniae type 4 strain	protein from coding region #1940.	PA	(GENO-) GENOME THERAPEUTICS CORP.
PN	WO20027721-A2.		Query Match	6.0%;
PD	03-OCT-2002.		Best Local Similarity	21.8%;
PA	(CHIR-) CHIRON SPA.		Pred. No.	7.1;
PA	Query Match	6.0%;	ID	ABU32051 standard; protein; 1137 AA.
PA	Best Local Similarity	24.4%;	DE	Protein encoded by Prokaryotic essential gene #17578.
RESULT	1392		DN	WO200277183-A2.
ID	AD210513	standard; protein; 403 AA.	PD	03-OCT-2002.
DE	P. gingivalis hypothetical	protein SEQ ID 296.	PA	(ELIT-) ELITRA PHARM INC.
PN	WO200519249-A2.		Query Match	6.0%;
PD	03-MAR-2005.		Best Local Similarity	18.6%;
PA	(UYFL) UNIV FLORIDA.		Pred. No.	13.1;
PA	Query Match	6.0%;	ID	ABO67057 standard; protein; 1138 AA.
PA	Best Local Similarity	21.9%;	DE	Klebsiella pneumoniae polypeptide seqid 13574.
RESULT	1393		DN	WO200277183-A2.
ID	ABG10541	standard; protein; 480 AA.	PD	26-AUG-2003.
DE	Novel human diagnostic	protein #10532.	PA	(GENO-) GENOME THERAPEUTICS CORP.
PN	WO200175067-A2.		Query Match	6.0%;
PD	11-OCT-2001.		Best Local Similarity	18.6%;
PA	(HYSE-)	HYSEQ INC.	Pred. No.	13.1;
PA	Query Match	6.0%;	ID	ADT60220 standard; protein; 294 AA.
PA	Best Local Similarity	20.5%;	DE	Plant Polypeptide, SEQ ID 10297.
RESULT	1394		DN	US2004216190-A1.
ID	ADL04919	standard; protein; 506 AA.	PD	28-OCT-2004.
DE	M. catarrhalis	protein #685.	PA	(KOVKA) KOVALIC D K.
PN	US6673110-B1.		Query Match	6.0%;
PD	06-JAN-2004.		Best Local Similarity	25.4%;
PA	(GENO-) GENOME THERAPEUTICS CORP.		Pred. No.	2.4;
PA	Query Match	6.0%;	ID	ABU38784 standard; protein; 295 AA.
PA	Best Local Similarity	19.9%;	DE	Protein encoded by Prokaryotic essential gene #23401.
RESULT	1395		DN	WO200277183-A2.
ID	ADS23302	standard; protein; 516 AA.	PD	03-OCT-2002.
DE	Bacterial polypeptide	#12425.	PA	(ELIT-) ELITRA PHARM INC.
PN	US200333675-A1.		Query Match	6.0%;
PD	18-DEC-2003.		Best Local Similarity	21.6%;
PA	(CROY/)	CAO Y.	Pred. No.	2.4;
PA	(HINK/)	HINKLE G J.	ID	AEP1231 standard; protein; 308 AA.
PA	(SLAT/)	SLATER S C.	DE	Murine trace amine associated receptor 7b SEQ ID NO:50.
PA	(CHEN/)	CHEN X.	DN	US200600941-A1.
PA	(GOLD/)	GOLDMAN B S.	PD	12-JAN-006.
PA	Query Match	6.0%;	PA	(EBEL/)
PA	Best Local Similarity	25.0%;	PA	(EBEL/)
RESULT	1396		PA	(HOEN/)
ID	ABO67632	standard; protein; 537 AA.	PA	(HORN/)
DE	Klebsiella pneumoniae polypeptide seqid 14149.		PA	(LIND/)
PA	Best Local Similarity	25.5%;	PA	(LIND/)
RESULT	1397		PA	(LINDMANN L.
ID	ABO788472	standard; protein; 333 AA.	PD	Score 83.5%; DB 10; Length 308;

DE Streptococcus agalactiae protein sequence, SEQ ID 866.	ID AAY85935 standard; protein; 318 AA.
PN FR2824074-A1.	DE S. pneumoniae derived protein #144.
PD 31-OCT-2002.	PN WO9806734-A1.
PA (INSP) INST PASTEUR.	PD 19-FEB-1998.
PA (CNRS) CNRS CENT NAT RECH SCI.	PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 6.0%; Score 83.5%; DB 8; Length 333;	Query Match 6.0%; Score 83%; DB 2; Length 318;
Best Local Similarity 21.4%; Pred. No. 2.8;	Best Local Similarity 24.4%; Pred. No. 3;
RESULT 1406	RESULT 1415
ID ADV79735 standard; protein; 333 AA.	ID ADK4461 standard; protein; 318 AA.
DE Streptococcus agalactiae protein, SEQ ID 866.	DB Streptococcus pneumoniae protein, Seq ID No 2976.
PN WO20022818-A2.	PN US6693703-B1.
PD 21-NOV-2002.	PD 02-MAR-2004.
PA (INSP) INST PASTEUR.	PA (GENO-) GENOME THERAPEUTICS CORP.
PA (CNRS) CNRS CENT NAT RECH SCI.	Query Match 6.0%; Score 83%; DB 8; Length 318;
Query Match 6.0%; Score 83.5%; DB 8; Length 333;	Best Local Similarity 24.4%; Pred. No. 3;
Best Local Similarity 21.4%; Pred. No. 2.8;	RESULT 1416
RESULT 1407	ID AAG71916 standard; protein; 319 AA.
ID ADV81883 standard; protein; 333 AA.	DE Human olfactory receptor polypeptide, SEQ ID NO: 1597.
DE Streptococcus agalactiae protein, SEQ ID 3024.	PN WO200127138-A2.
PN WO20022818-A2.	PD 19-APR-2001.
PD 21-NOV-2002.	PA (DIGIT-) DIGISCIENTS.
PA (INSP) INST PASTEUR.	PA (YEDA) YEDA RES & DEV CO LTD.
PA (CNRS) CNRS CENT NAT RECH SCI.	Query Match 6.0%; Score 83%; DB 4; Length 319;
Query Match 6.0%; Score 83.5%; DB 8; Length 333;	Best Local Similarity 20.6%; Pred. No. 3;
Best Local Similarity 21.4%; Pred. No. 2.8;	RESULT 1417
RESULT 1408	ID AAB46399 standard; protein; 321 AA.
ID AAR97904 standard; protein; 618 AA.	DE Human OLFXV protein.
DE DmORF1 potassium channel protein.	PN DE19937839-A1.
PN WO961320-A1.	PD 15-FEB-2001.
PD 09-MAY-1996.	PA (BRUE-) BRUESS M.
PA (AMCY) AMERICAN CYANAMID CO.	PA (BOEN/) BOENISCH H.
Query Match 6.0%; Score 83.5%; DB 2; Length 618;	Query Match 6.0%; Score 83%; DB 4; Length 321;
Best Local Similarity 19.9%; Pred. No. 6.6;	Best Local Similarity 20.0%; Pred. No. 3;
RESULT 1409	RESULT 1418
ID ARU07616 standard; protein; 618 AA.	ID ABP95927 standard; protein; 321 AA.
DE Drosophila melanogaster potassium ion channel ORF1 (DmORF1) protein.	DE Human GPCR polyPeptide SEQ ID NO 664.
PN WO20015106-A2.	PN WO200216548-A2.
PD 23-AUG-2001.	PD 28-FEB-2002.
PA (BADI) BASF CORP.	PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.0%; Score 83.5%; DB 4; Length 618;	Query Match 6.0%; Score 83%; DB 5; Length 321;
Best Local Similarity 19.9%; Pred. No. 6.6;	Best Local Similarity 20.6%; Pred. No. 3;
RESULT 1410	RESULT 1419
ID ABG30123 standard; protein; 1027 AA.	ID ADU24127 standard; protein; 321 AA.
DE Novel human diagnostic protein #30114.	DE Human aspartic peptidase enzyme #119.
PN WO200175067-A2.	DE US2001219659-A1.
PD 11-OCT-2001.	PD 04-NOV-2004.
PA (HYSE-) HYSEQ INC.	PA (DAYA-) DAY A. G.
Query Match 6.0%; Score 83.5%; DB 4; Length 1027;	PA (ESTE-) ESTELL D. A.
Best Local Similarity 19.8%; Pred. No. 13;	PA (LYON-) LYONS E. H.
RESULT 1411	PA (YAOJ-) YAO J.
ID ABP28293 standard; protein; 1090 AA.	Query Match 6.0%; Score 83%; DB 8; Length 321;
DE Protein encoded by Prokaryotic essential gene #13820.	Best Local Similarity 20.6%; Pred. No. 3;
PN WO20027183-A2.	RESULT 1420
PD 03-OCT-2002.	ID ADR9641 standard; protein; 336 AA.
PA (ELIT-) ELITRA PHARM INC.	DE Novel S. pneumoniae protein sequence, SEQ ID 5076.
Query Match 6.0%; Score 83.5%; DB 6; Length 1090;	PN US6800744-B1.
Best Local Similarity 18.5%; Pred. No. 14;	PD 05-OCT-2004.
RESULT 1412	PA (GENO-) GENOME THERAPEUTICS CORP.
ID AAG44538 standard; protein; 250 AA.	Query Match 6.0%; Score 83%; DB 8; Length 336;
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55802.	Best Local Similarity 24.4%; Pred. No. 3.2;
PN BP1033405-A2.	RESULT 1421
PD 06-SEP-2000.	ID AFA60311 standard; protein; 336 AA.
Query Match 6.0%; Score 83%; DB 3; Length 250;	DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:5076.
Best Local Similarity 21.7%; Pred. No. 2.2;	PN US2005136404-A1.
RESULT 1413	PD 23-JUN-2005.
ID AAC66371 standard; protein; 305 AA.	PA (DOUC-) DOUCETTE-STAMM L A.
DE Human olfactory receptor-like protein OLF3 #2.	PA (BUSH-) BUSH D.
PN WO200155179-A2.	Query Match 6.0%; Score 83%; DB 9; Length 336;
PD 02-AUG-2001.	Best Local Similarity 24.4%; Pred. No. 3.2;
PA (CURA-) CURAGEN CORP.	RESULT 1422
Query Match 6.0%; Score 83%; DB 4; Length 305;	ID ABU43979 standard; protein; 355 AA.
Best Local Similarity 20.6%; Pred. No. 2.8;	DE Protein encoded by Prokaryotic essential gene #29506.
RESULT 1414	PN WO20027183-A2.

PD 03-OCT-2002.
 PA (ELITE-) ELITRA PHARM INC. Query Match 6.0%; Score 83; DB 6; Length 355;
 Best Local Similarity 23.0%; Pred. No. 3.5%;
 RESULT 1423
 ID AB062213 standard; protein; 417 AA.
 DE Klebsiella pneumoniae polypeptide seqid 8730.
 PN US6610336-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP. Query Match 6.0%; Score 83; DB 7; Length 417;
 Best Local Similarity 20.8%; Pred. No. 4.4%;
 RESULT 1424
 ID AAY66647 standard; protein; 455 AA.
 DE Membrane-bound protein PRO32.
 PN WO963088-A2.
 PD 09-DEC-1999.
 PA (GBTM-) GENENTECH INC. Query Match 6.0%; Score 83; DB 3; Length 455;
 Best Local Similarity 19.8%; Pred. No. 4.9%;
 RESULT 1425
 ID AAB96670 standard; protein; 490 AA.
 DE Putative P. abyssi succinyl-CoA synthetase #5.
 PN FR2792651-A1.
 PD 27-OCT-2000.
 PA (CNRS) CNRS CENT NAT RECH SCI. (IFRE-) IFREMER INST FR RECH EXPL MER. Query Match 6.0%; Score 83; DB 4; Length 490;
 Best Local Similarity 23.6%; Pred. No. 5.5%;
 RESULT 1426
 ID ABO70524 standard; protein; 542 AA.
 DE Pseudomonas aeruginosa polypeptide #2699.
 PN US6551195-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP. Query Match 6.0%; Score 83; DB 7; Length 542;
 Best Local Similarity 20.2%; Pred. No. 6.3%;
 RESULT 1427
 ID ADA33498 standard; protein; 632 AA.
 DE Acinetobacter baumannii protein #659.
 PN US6562958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP. Query Match 6.0%; Score 83; DB 6; Length 632;
 Best Local Similarity 25.1%; Pred. No. 7.7%;
 RESULT 1428
 ID ABB65640 standard; protein; 774 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 23712.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY. Query Match 6.0%; Score 83; DB 4; Length 774;
 Best Local Similarity 22.4%; Pred. No. 10%;
 RESULT 1429
 ID ADG35811 standard; protein coupled receptor seq id 43.
 DE Drosophila G protein coupled receptor seq id 43.
 PN US2003092124-A1.
 PD 15-MAY-2003.
 PA (APPL-) APPLERA CORP. Query Match 6.0%; Score 83; DB 7; Length 774;
 Best Local Similarity 22.4%; Pred. No. 10%;
 RESULT 1430
 ID AAE38109 standard; protein; 802 AA.
 DE Fruit fly G protein-coupled receptor (GPCR) protein #48.
 PN WO2003052078-A2.
 PD 26-JUN-2003.
 PA (SYGN) SINGENTA PARTICIPATIONS AG. Query Match 6.0%; Score 83; DB 7; Length 802;
 Best Local Similarity 22.4%; Pred. No. 11%;
 RESULT 1432
 ID ABP70524 standard; protein; 2159 AA.
 DE Maize DEK1 from B73.
 PN WO2003011015-A2.
 PD 13-FEB-2003.
 PA (PION-) PIONEER HI-BRED INT INC. Query Match 6.0%; Score 83; DB 6; Length 2159;
 Best Local Similarity 20.6%; Pred. No. 42%;
 RESULT 1433
 ID ADT57399 standard; protein; 2159 AA.
 DE Plant polypeptide, SEQ ID 7476.
 PN US2004216190-A1.
 PD 28-OCT-2004.
 PA (KOVA/) KOVALIC D K. Query Match 6.0%; Score 83; DB 8; Length 2159;
 Best Local Similarity 20.6%; Pred. No. 42%;
 RESULT 1434
 ID ADS43623 standard; protein; 391 AA.
 DE Bacterial polypeptide #22053.
 PN US2003233675-A1.
 PA (CAOV/) CAO Y.
 PA (HINKL/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 5.9%; Score 82.5; DB 8; Length 391;
 Best Local Similarity 23.2%; Pred. No. 4.6%;
 RESULT 1435
 ID ABU28011 standard; protein; 395 AA.
 DE Protein encoded by Prokaryotic essential gene #113538.
 PN WO200327183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC. Query Match 5.9%; Score 82.5; DB 6; Length 395;
 Best Local Similarity 19.7%; Pred. No. 4.6%;
 RESULT 1436
 ID AAW21009 standard; protein; 461 AA.
 DE H. pylori cell envelope transporter protein, hp5e11726orf7.
 PN WO9610893-A1.
 PD 19-DEC-1996.
 PA (ASTR) ASTRA AB. Query Match 5.9%; Score 82.5; DB 2; Length 461;
 Best Local Similarity 21.5%; Pred. No. 5.7%;
 RESULT 1437
 ID ABO63393 standard; protein; 492 AA.
 DE Pseudomonas aeruginosa polypeptide #1568.
 PN US65511795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP. Query Match 5.9%; Score 82.5; DB 7; Length 492;
 Best Local Similarity 19.1%; Pred. No. 6.3%;
 RESULT 1438
 ID ADN18812 standard; protein; 596 AA.
 DE Bacterial polypeptide #1465.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOV/) CAO Y.
 PA (HINKL/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 5.9%; Score 82.5; DB 8; Length 596;
 Best Local Similarity 20.6%; Pred. No. 8.1%;
 RESULT 1439
 ID ABG06358 standard; protein; 875 AA.
 DE Novel human diagnostic protein #6549.
 PN WO200175067-A2.
 PD 11-OCT-2001.

PA	(HYSE-) HYSEQ INC.	5.9%	Score 82.5; DB 4;	Length 875;	Best Local Similarity 22.8%; Pred. No. 3.6;
Best Local Similarity	26.0%; Pred. No. 14;				RESULT 1448
RESULT 1440	ID ADJ69204 standard; protein; 1457 AA.				ID ABB10684 standard; protein; 356 AA.
ID	DE Human heart mitochondrial protein as a therapeutic target SeqID1010.				DB A. thaliana PUP1 protein.
DE	PN WO200387768-A2.				PN DE119907209-A1.
PD	23-OCT-2003				PD 24-AUG-2000
PA	(MITO-) MITOKOR.				PA (FROM /) FROMMER W.
PA	(BUCK-) BUCK INST AGE RES.				Query Match 5.9%; Score 82; DB 3; Length 356;
Query Match	Score 82.5; DB 7;	Length 1457;			Best Local Similarity 19.4%; Pred. No. 4.6;
Best Local Similarity	26.0%; Pred. No. 28;				RESULT 1449
RESULT 1441	ID ADJ69205 standard; protein; 1457 AA.				ID ABB1157 standard; protein; 356 AA.
ID	DE Human heart mitochondrial protein as a therapeutic target SeqID1011.				DE Herbicidally active polypeptide SEQ ID NO 368.
PN	WO200387768-A2.				PN WO200310210-A2.
PD	23-OCT-2003				PD 07-FEB-2004.
PA	(MITO-) MITOKOR.				PA (FARB 1) BAYER AG.
PA	(BUCK-) BUCK INST AGE RES.				Query Match 5.9%; Score 82; DB 5; Length 356;
Query Match	Score 82.5; DB 7;	Length 1457;			Best Local Similarity 19.4%; Pred. No. 4.6;
Best Local Similarity	26.0%; Pred. No. 28;				RESULT 1450
RESULT 1442	ID ADJ58460 standard; protein; 1457 AA.				ID ABU8157 standard; protein; 417 AA.
ID	DE BAB13458.1(P450G5) protein.				DE Protein encoded by prokaryotic essential gene #13684.
PN	WO2004011648-A2.				PN WO200277183-A2.
PD	05-FEB-2004				PD 03-OCT-2002.
PA	(INPH-) INPHARMATICA LTD.				PA (ELIT-) ELITRA PHARM INC.
Query Match	5.9%; Score 82.5; DB 8;	Length 1457;			Query Match 5.9%; Score 82; DB 6; Length 417;
Best Local Similarity	26.0%; Pred. No. 28;				Best Local Similarity 27.1%; Pred. No. 5.7;
RESULT 1443	ID ADC1246 standard; protein; 2548 AA.				RESULT 1451
ID	DE Human novel polypeptide sequence, SEQ ID NO:1328.				ID ADX68336 standard; protein; 440 AA.
PN	WO200329271-A2.				DE Plant full length insert polypeptide seqid 39179.
PD	10-APR-2003.				DE US2004034888-A1.
PA	(HYSE-) HYSEQ INC.				PA (LIUJ /) LIU J.
Query Match	5.9%; Score 82.5; DB 7;	Length 2548;			PA (ZHOU /) ZHOU Y.
Best Local Similarity	26.0%; Pred. No. 60;				PA (KOVALIC /) KOVALIC D K.
RESULT 1444	ID ABO84919 standard; protein; 219 AA.				PA (SCRE /) SCREEN S E.
ID	DE Human cancer-associated protein (CAP) HP07-069.				PA (TABA /) TABASKA J E.
PN	WO2004058146-A2.				PA (CAOY /) CAO Y.
PD	15-JUL-2004.				Query Match 5.9%; Score 82; DB 8; Length 440;
PA	(SAGR-) SAGRES DISCOVERY INC.				Best Local Similarity 24.4%; Pred. No. 6.1;
Query Match	5.9%; Score 82; DB 8;	Length 219;			RESULT 1452
Best Local Similarity	22.1%; Pred. No. 2.3;				ID ADK16201 standard; protein; 465 AA.
RESULT 1445	ID AAB87783 standard; protein; 299 AA.				DE Nanoarchaeum equitans cancer-associated (CA) protein #426.
ID	DE Rat T2R03 amino acid sequence SEQ ID NO:81.				PN WO2003093434-A2.
PN	WO200118050-A2.				PD 13-NOV-2003.
PD	15-MAR-2001.				PA (DIVE -) DIVERSA CORP.
PA	(REGC) UNIV CALIFORNIA.				Query Match 5.9%; Score 82; DB 8; Length 465;
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.				Best Local Similarity 23.7%; Pred. No. 6.6;
Query Match	5.9%; Score 82; DB 4;	Length 299;			RESULT 1453
Best Local Similarity	22.8%; Pred. No. 3.6;				ID ABO81608 standard; protein; 474 AA.
RESULT 1446	ID ADJ84452 standard; protein; 299 AA.				DE Pseudomonas aeruginosa polypeptide #13783.
ID	DE Rat T2R G-protein coupled receptor seq id 5.				PN US6551795-B1.
PN	US2004038312-A1.				PD 22-APR-2003.
PD	26-FEB-2004.				PA (GENO-) GENOME THERAPEUTICS CORP.
PA	(DUKE /) ZUKER C S.				Query Match 5.9%; Score 82; DB 7; Length 474;
PA	(ADLE /) ADLER J E.				Best Local Similarity 20.1%; Pred. No. 6.8;
PA	(HOON /) HOON M.				RESULT 1454
PA	(RYBA /) RYBA N.				ID ADY1345 standard; protein; 478 AA.
PA	(MUEL /) MUELLER K.				DE Plant full length insert polypeptide seqid 69270.
Query Match	5.9%; Score 82; DB 8;	Length 299;			PN US2004034888-A1.
Best Local Similarity	22.8%; Pred. No. 3.6;				PD 19-FEB-2004.
RESULT 1447	ID ADR29142 standard; protein; 299 AA.				PA (LIUJ /) LIU J.
ID	DE Taste receptor modulation-related rat T2R03 protein sequence SeqID011.				PA (ZHOU /) ZHOU Y.
PN	WO200406191-A2.				PA (KOVALIC /) KOVALIC D K.
PD	19-AUG-2004.				PA (SCRE /) SCREEN S E.
PA	(SEN0- SENOMYX INC.				PA (CAOY /) TABASKA J E.
Query Match	5.9%; Score 82; DB 8;	Length 299;			PA (CAOY /) CAO Y.
Best Local Similarity	22.8%; Pred. No. 3.6;				Query Match 5.9%; Score 82; DB 8; Length 478;
RESULT 1448	ID ADR29142 standard; protein; 573 AA.				Best Local Similarity 23.3%; Pred. No. 6.8;
ID	DE Bacterial polypeptide #5872.				RESULT 1455
PN	US2003233675-A1.				ID ADN23219 standard; protein.
PD	18-DEC-2003.				DE US2003233675-A1.
PA	(CROY /) CAO Y.				PA (CROY /) CAO Y.

PA	(HINK/) HINKLE G J.	Best Local Similarity	20.2%;	Pred. No. 23;
PA	(CHEN/) SLATER S C.	RESULT 1463		
PA	(CHEN/) CHEN X.	ID ADE56876 Standard; protein: 1168 AA.		
PA	(GOLD/) GOLDMAN B S.	ID Human Protein 043306, SEQ ID NO 2731.		
Query Match	5.9%; Score 82; DB 8; Length 573;	DE		
Best Local Similarity	18.5%; Pred. No. 8.8;	PN		
RESULT 1456		WO2003016475-A2.		
ID	ADN23218 standard; protein: 573 AA.	PD		
DE	Bacterial polypeptide #5871.	PA		
PN	US2003233675-A1.	(PARB) BAYER AG.		
PD	18-DEC-2003.	Query Match	5.9%;	Score 82; DB 7; Length 1168;
PA	(CRAO/) CAO Y.	Best Local Similarity	20.2%;	Pred. No. 23;
PA	(HINK/) HINKLE G J.	RESULT 1464		
PA	(SLAT/) SLATER S C.	ID ADQ9850 Standard; protein: 1168 AA.		
PA	(CHEN/) CHEN X.	DE Antagonist of cell cycle progression polypeptide #140.		
PA	(GOLD/) GOLDMAN B S.	PN WO2004063362-A2.		
Query Match	5.9%; Score 82; DB 8; Length 573;	PD 29-JUL-2004.		
Best Local Similarity	18.5%; Pred. No. 8.8;	PA (CYCL-) CYCLACEL LTD.		
RESULT 1457		Query Match	5.9%;	Score 82; DB 8; Length 1168;
ID	ABU5193 standard; protein: 1139 AA.	Best Local Similarity	20.2%;	Pred. No. 23;
DE	Protein encoded by Prokaryotic essential gene #35720.	RESULT 1465		
PN	W020027183-A2.	ID ADX9516 Standard; protein: 1168 AA.		
PD	03-OCT-2002.	DE Human adenylyl cyclase 6 (ADCY6) protein.		
PA	(ELIT-) ELITRA PHARM INC.	PN WO2005017121-A2.		
Query Match	5.9%; Score 82; DB 6; Length 1139;	PD 24-FEB-2005.		
Best Local Similarity	19.5%; Pred. No. 23;	PA (EXEL-) EXBLIXIS INC.		
RESULT 1458		Query Match	5.9%;	Score 82; DB 9; Length 1168;
ID	AAE04312 standard; protein: 1167 AA.	Best Local Similarity	20.2%;	Pred. No. 23;
DE	Human modified cardiac adenylylcyclase VI (ACVI) isoform.	RESULT 1466		
PN	WO200148164-A2.	ID ADK46612 Standard; protein: 199 AA.		
PD	05-JUL-2001.	DE Streptococcus pneumoniae protein, Seq ID No 3127.		
PA	(RBCG) UNIV CALIFORNIA.	PN US6699703-B1.		
Query Match	5.9%; Score 82; DB 4; Length 1167;	PD 02-MAR-2004.		
Best Local Similarity	20.2%; Pred. No. 23;	PA (GENO-) GENOME THERAPEUTICS CORP.		
RESULT 1459		Query Match	5.9%;	Score 81.5%; DB 8; Length 199;
ID	ABG32870 standard; protein: 1167 AA.	Best Local Similarity	20.2%;	Pred. No. 23;
DE	Chimaeric Adenylylcyclase Isoform 6, AC-VI.	RESULT 1467		
PN	US2002103147-A1.	ID ABU02196 Standard; protein: 205 AA.		
PD	01-AUG-2002.	DE S. pneumoniae type 4 strain protein from coding region #1774.		
PA	(HRMM/) HAMMOND H K.	PN WO200277021-A2.		
PA	(INSE/) INSEL P A.	PD 03-OCT-2002.		
PA	(PING/) PING P.	PA (CHIR-) CHIRON SPA.		
PA	(POST/) POST S R.	PA (GENO-) INST GENOMIC RES.		
PA	(GAOM/) GAO M.	Query Match	5.9%;	Score 81.5%; DB 6; Length 205;
Query Match	5.9%; Score 82; DB 5; Length 1167;	Best Local Similarity	20.2%;	Pred. No. 2.4;
Best Local Similarity	20.2%; Pred. No. 23;	RESULT 1468		
RESULT 1460		ID AAY81546 Standard; protein: 206 AA.		
ID	AAW30599 standard; protein: 1168 AA.	DE Streptococcus pneumoniae type 4 protein sequence #46.		
DE	Human cardiac adenylyl cyclase.	PN WO200006737-A2.		
PN	WO99015457-A1.	PD 10-FEB-2000.		
PD	14-JAN-1999.	PA (MICR-) MICROBIAL TECHNICS LTD.		
PA	(CORT-) COR THERAPEUTICS INC.	Query Match	5.9%;	Score 81.5%; DB 3; Length 206;
Query Match	5.9%; Score 82; DB 2; Length 1168;	Best Local Similarity	20.2%;	Pred. No. 2.5;
Best Local Similarity	20.2%; Pred. No. 23;	RESULT 1469		
RESULT 1461		ID ADR96056 Standard; protein: 208 AA.		
ID	AAE04311 standard; protein: 1168 AA.	DE Novel S. pneumoniae protein sequence, SEQ ID 4691.		
DE	Human cardiac adenylylcyclase VI (ACVI) isoform #12.	PN US6800744-81.		
PN	WO200146164-A2.	PD 05-OCT-2004.		
PD	05-JUL-2001.	PA (GENO-) GENOME THERAPEUTICS CORP.		
PA	(RBCG) UNIV CALIFORNIA.	Query Match	5.9%;	Score 81.5%; DB 8; Length 208;
Query Match	5.9%; Score 82; DB 4; Length 1168;	Best Local Similarity	20.2%;	Pred. No. 2.5;
Best Local Similarity	20.2%; Pred. No. 23;	RESULT 1470		
RESULT 1462		ID AEA59926 Standard; protein: 208 AA.		
ID	ABG32869 standard; protein: 1168 AA.	DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4691.		
DE	Human Adenylylcyclase Isoform 6, AC-VI, #2.	PN US2005136104-A1.		
PN	US2002103147-A1.	PD 23-JUN-2005.		
PD	01-AUG-2002.	PA (DOUC/) DOUCETTE-STANN L A.		
PA	(HAMM/) HAMMOND H K.	PA (BUSH/) BUSH D.		
PA	(INSE/) INSEL P A.	Query Match	5.9%;	Score 81.5%; DB 9; Length 208;
PA	(PING/) PING P.	Best Local Similarity	20.2%;	Pred. No. 2.5;
PA	(POST/) POST S R.	RESULT 1471		
PA	(GAOM/) GAO M.	ID ABU41035 Standard; protein: 278 AA.		
Query Match	5.9%; Score 82; DB 5; Length 1168;	DE Protein encoded by Prokaryotic essential gene #26562.		
		PN WO20027183-A2.		
		PD 03-OCT-2002.		

ID AAE21184 standard; protein; 515 AA.
 DE PN200212340-A2.
 PD 14-FEB-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.8%; Score 81; DB 5;
 Best Local Similarity 17.8%; Pred. No. 9.9;
 RESULT 1490
 ID ABJ37907 standard; protein; 515 AA.
 DE NOVIX protein sequence SEQ ID No 60.
 PN WO200281517-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.8%; Score 81; DB 6;
 Best Local Similarity 17.8%; Pred. No. 9.9;
 RESULT 1491
 ID ADQ66916 standard; protein; 515 AA.
 DE Novel human protein sequence #1889.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 5.8%; Score 81; DB 8;
 Best Local Similarity 17.8%; Pred. No.. 9.9;
 RESULT 1492
 ID ABO84591 standard; protein; 515 AA.
 DE Human cancer-associated protein HP17-001.2.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 5.8%; Score 81; DB 8;
 Best Local Similarity 17.8%; Pred. No. 9.9;
 RESULT 1493
 ID ADH58563 standard; protein; 516 AA.
 DE Human Na+-independent transporter-related transporter protein.
 PN WO2003076644-A2.
 PD 18-SEP-2003.
 PA (APPL-) APPLERA CORP.
 Query Match 5.8%; Score 81; DB 7;
 Best Local Similarity 17.8%; Pred. No. 9.9;
 RESULT 1494
 ID ADN23220 standard; protein; 544 AA.
 DE Bacterial polypeptide #5873.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CROY-) CAO Y.
 PA (HINK-) HINKLE G J.
 PA (SLAT-) SLATER S C.
 PA (CHEN-) CHEN X.
 PA (GOLD-) GOLDMAN B S.
 Query Match 5.8%; Score 81; DB 8;
 Best Local Similarity 23.0%; Pred. No. 11;
 RESULT 1495
 ID ABB64860 standard; protein; 875 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 21372.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Query Match 5.8%; Score 81; DB 4;
 Best Local Similarity 20.9%; Pred. No. 20;
 RESULT 1496
 ID ABU39716 standard; protein; 1102 AA.
 DE Protein encoded by Prokaryotic essential gene #25243.
 PN WO200271183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.8%; Score 81; DB 6;
 Best Local Similarity 20.0%; Pred. No. 28;
 RESULT 1497
 ID ADY52908 standard; protein; 260 AA.
 DE Nodularia spumigena ketocarotenoid-related ketolase protein - SEQ ID 4.
 PN WO2005019461-A2.
 PD 03-MAR-2005.
 PA (SUNG-) SUNGENE GMBH & CO KGAA.

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OM protein - protein search, using sw model

Run on: August 28, 2006, 17:41:45 ; Search time 50 Seconds

(without alignments)

465.663 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

Sequence: 1 MWWFQQGLSFLPSALVITWS.....YDTAPCPINNERTRLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDBS3/prodata/2/iaaa/5_COMBO.pep:*
- 2: /EMC_Celerra_SIDBS3/prodata/2/iaaa/6_COMBO.pep:*
- 3: /EMC_Celerra_SIDBS3/prodata/2/iaaa/7_COMBO.pep:*
- 4: /EMC_Celerra_SIDBS3/prodata/2/iaaa/H_COMBO.pep:*
- 5: /EMC_Celerra_SIDBS3/prodata/2/iaaa/PCTOS_COMBO.pep:*
- 6: /EMC_Celerra_SIDBS3/prodata/2/iaaa/RE_COMBO.pep:*
- 7: /EMC_Celerra_SIDBS3/prodata/2/iaaa/batchfile11.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1392	100.0	266	2	US-09-991-181-23	Sequence 23 , App1
2	1392	100.0	266.	2	US-09-990-444-23	Sequence 23 , App1
3	1392	100.0	266.	2	US-09-997-333-23	Sequence 23 , App1
4	1392	100.0	266.	2	US-09-992-598-23	Sequence 23 , App1
5	1392	100.0	266.	2	US-09-988-726-23	Sequence 23 , App1
6	1392	100.0	266.	3	US-09-997-514-23	Sequence 23 , App1
7	1392	100.0	266.	3	US-09-989-728-23	Sequence 23 , App1
8	1392	100.0	266.	3	US-09-997-349-23	Sequence 23 , App1
9	1392	100.0	266.	3	US-09-997-653-23	Sequence 23 , App1
10	1392	100.0	266.	3	US-09-988-293A-23	Sequence 23 , App1
11	1392	99.7	266.	2	US-09-993-600A-190	Sequence 190 , App
12	1398	99.7	267	2	US-09-663-600A-96	Sequence 96 , App
13	595.5	42.8	172	2	US-09-663-600A-20	Sequence 20 , App1
14	479.5	34.4	238	2	US-09-724-864-38	Sequence 2 , App1
15	355	25.7	69	2	US-09-663-600A-130	Sequence 130 , App
16	358	25.7	69	2	US-09-663-600A-224	Sequence 224 , App
17	118	8.5	21	2	US-08-905-223-20	Sequence 20 , App1
18	118	8.5	21	2	US-09-247-155-20	Sequence 20 , App1
19	118	8.5	21	2	US-09-663-600A-20	Sequence 20 , App1
20	118	8.5	21	2	US-09-621-976-2	Sequence 2 , App1
21	118	8.5	21	2	US-09-513-999C-2	Sequence 2 , App1
22	118	8.5	21	2	US-09-471-276-2	Sequence 2 , App1
23	118	8.5	21	2	US-09-903-190-20	Sequence 20 , App1
24	91.5	6.6	291	2	US-09-107-532A-4147	Sequence 4147 , App
25	91.5	6.6	387	2	US-09-722-870-14	Sequence 14 , App
26	90	6.5	283	2	US-09-602-787A-588	Sequence 588 , App

27	90	6.5	396	2	US-09-248-796A-20434	Sequence 20434 , A
28	89	6.4	344	2	US-10-749-293A-16383	Sequence 2651 , Ap
29	88	6.3	1165	1	US-08-240-357-2	Sequence 2 , App1
30	88	6.2	356	2	US-09-134-000C-1914	Sequence 4 , App1
31	86.5	6.1	579	2	US-09-786-581A-4	Sequence 2 , App1
32	85.5	6.1	582	2	US-09-786-581A-2	Sequence 2 , App1
33	85	6.1	419	2	US-09-948-774-2	Sequence 2 , App1
34	85	6.1	1180	2	US-08-726-214-12	Sequence 12 , App1
35	85	6.1	296	2	US-09-134-000C-6205	Sequence 6205 , Ap
36	84.5	6.1	356	2	US-10-144-929-114	Sequence 114 , App
37	84.5	6.1	453	2	US-09-591-181-73	Sequence 73 , App1
38	84.5	6.1	453	2	US-09-990-444-73	Sequence 73 , App1
39	84.5	6.1	453	2	US-09-997-514-73	Sequence 73 , App1
40	84.5	6.1	453	2	US-09-997-333-73	Sequence 73 , App1
41	84.5	6.1	453	2	US-09-992-538-73	Sequence 73 , App1
42	84.5	6.1	453	2	US-09-989-039A-13574	Sequence 73 , App1
43	84	6.0	506	2	US-09-328-352-8001	Sequence 8001 , Ap
44	84	6.0	506	2	US-09-540-336-265	Sequence 2605 , Ap
45	84	6.0	537	2	US-09-989-726-73	Sequence 14149 , A
46	84	6.0	602	2	US-09-252-991A-22527	Sequence 22527 , A
47	84	6.0	720	2	US-09-252-991A-19581	Sequence 19581 , A
48	84	6.0	1138	2	US-09-989-233A-73	Sequence 13574 , A
49	84	6.0	618	2	US-09-332-312-2	Sequence 2 , App1
50	84	6.0	318	2	US-09-583-110-2976	Sequence 2976 , Ap
51	84	6.0	336	2	US-09-107-039A-5076	Sequence 5076 , Ap
52	84	6.0	602	2	US-09-252-991A-19270	Sequence 19270 , A
53	84	6.0	542	2	US-09-489-039A-14149	Sequence 14149 , A
54	84	6.0	632	2	US-09-328-352-4785	Sequence 4785 , Ap
55	83.5	6.0	618	2	US-09-328-352-4785	Sequence 4785 , Ap
56	83	6.0	318	2	US-09-583-110-2976	Sequence 2976 , Ap
57	83	6.0	336	2	US-09-107-039A-5076	Sequence 5076 , Ap
58	83	6.0	417	2	US-09-489-039A-14149	Sequence 14149 , A
59	83	6.0	632	2	US-09-252-991A-19270	Sequence 19270 , A
60	83	6.0	632	2	US-09-489-039A-14149	Sequence 14149 , A
61	82.5	5.9	492	2	US-09-252-991A-18139	Sequence 18139 , A
62	82	5.9	299	2	US-09-593-634-5	Sequence 5 , App1
63	82	5.9	299	2	US-10-127-81	Sequence 8756 , Ap
64	82	5.9	474	2	US-09-252-991A-20354	Sequence 30354 , A
65	82	5.9	574	2	US-09-248-796A-20154	Sequence 20154 , A
66	82	5.9	664	2	US-09-248-796A-17191	Sequence 17191 , A
67	82	5.9	1094	2	US-09-949-016-8755	Sequence 8755 , Ap
68	82	5.9	1094	2	US-09-949-016-8756	Sequence 8756 , Ap
69	82	5.9	1147	2	US-09-949-016-8861	Sequence 8861 , Ap
70	82	5.9	1168	2	US-09-474-70-76-2	Sequence 2 , App1
71	82	5.9	1168	2	US-09-472-667-11	Sequence 11 , App1
72	82	5.9	1168	2	US-10-501-000-2	Sequence 2 , App1
73	82	5.9	1168	2	US-10-501-000-2	Sequence 2 , App1
74	81.5	5.9	199	2	US-09-583-110-3127	Sequence 3127 , Ap
75	81.5	5.9	205	2	US-09-769-487-46	Sequence 46 , Ap
76	81.5	5.9	208	2	US-09-107-433-4691	Sequence 4691 , Ap
77	81.5	5.9	280	2	US-09-543-881A-6175	Sequence 6175 , Ap
78	81.5	5.9	503	2	US-09-328-352-4763	Sequence 32663 , A
79	81	5.8	323	2	US-09-328-352-6181	Sequence 6181 , Ap
80	81	5.8	394	2	US-10-154-419-28	Sequence 28 , App1
81	81	5.8	425	2	US-09-489-089-8209	Sequence 8209 , Ap
82	81	5.8	298	2	US-09-489-039A-11920	Sequence 11920 , A
83	80.5	5.8	359	2	US-09-828-533A-14	Sequence 14 , App1
84	80.5	5.8	370	2	US-09-328-523A-74	Sequence 74 , App1
85	80.5	5.8	411	2	US-09-134-001C-3239	Sequence 3239 , Ap
86	80.5	5.8	607	1	US-07-879-617A-12	Sequence 12 , App1
87	80.5	5.8	607	1	US-08-677-724A-9	Sequence 1 , App1
88	80.5	5.8	834	1	US-08-677-724A-10	Sequence 10 , App1
89	80.5	5.8	834	1	US-09-097-053-10	Sequence 9 , App1
90	80.5	5.8	834	2	US-09-134-001C-3239	Sequence 10 , App1
91	80.5	5.8	834	2	US-09-097-053-10	Sequence 10 , App1
92	80	5.7	221	2	US-10-094-749-2202	Sequence 2202 , Ap
93	80	5.7	292	2	US-09-543-110-4056	Sequence 4530 , Ap
94	80	5.7	307	2	US-09-252-991A-18010	Sequence 18010 , A
95	80	5.7	308	2	US-09-252-991A-18010	Sequence 18010 , A
96	80	5.7	325	2	US-09-712-768-2	Sequence 2 , App1
97	80	5.7	241	2	US-09-328-332-7159	Sequence 7159 , Ap
98	79.5	5.7	241	2	US-09-328-332-7159	Sequence 7159 , Ap
99	79.5	5.7	274	2	US-09-902-540-14253	Sequence 14253 , A

100	79.5	308	2	US-09-328-352-7092	Sequence 7092, AP	173	74.5	384	2	US-09-248-796A-20119		
101	79.5	315	2	US-09-352-4864	Sequence 4864, AP	174	74.5	388	2	US-09-949-016-7331		
102	79.5	5.7	315	2	US-09-248-796A-15178	Sequence 15178, AP	175	74.5	5.4	405	2	US-09-719-0888B-3
103	79.5	5.7	483	2	US-09-488-039A-7429	Sequence 7429, AP	176	74.5	5.4	407	2	US-09-364-425B-23
104	79.5	5.7	831	1	US-08-677-730A-11	Sequence 11, App1	177	74.5	436	7	543201-10	
105	79.5	5.7	831	1	US-09-097-053-11	Sequence 11, App1	178	74.5	5.4	443	2	US-09-328-552-7069
106	79.5	5.7	298	2	US-09-438-185A-545	Sequence 545, App1	179	74.5	5.4	475	2	US-09-248-796A-20067
107	79.5	5.7	307	2	US-09-303-518D-404	Sequence 404, App1	180	74.5	5.4	556	2	US-09-248-796A-20229
108	79.5	5.7	491	1	US-09-512-681A-4195	Sequence 4195, App1	181	74.5	5.4	601	1	US-08-194-738-2
109	79.5	5.7	600	2	US-09-134-0000-5654	Sequence 5694, AP	182	74.5	5.4	824	2	US-09-605-703B-358
110	79.5	5.6	670	2	US-09-488-039A-7251	Sequence 7251, AP	183	74.5	5.4	832	2	US-09-605-703B-356
111	78.5	5.6	320	4	US-10-038-895A-5	Sequence 5, App1	184	74.5	5.4	1798	2	US-09-327-767-6233
112	78.5	5.6	473	2	US-09-543-681A-7980	Sequence 7980, AP	185	74.5	5.4	2410	2	US-09-227-767-44775
113	78.5	5.6	793	2	US-09-900-237-18	Sequence 18, App1	186	74	5.3	173	2	US-09-248-796A-2033
114	78.5	5.6	832	2	US-08-677-730A-12	Sequence 12, App1	187	74	5.3	262	2	US-09-328-332-6226
115	78.5	5.6	832	2	US-09-097-053-12	Sequence 12, App1	188	74	5.3	280	2	US-09-198-452-A-889
116	78	5.6	221	2	US-09-248-796A-16814	Sequence 16814, A	189	74	5.3	829	2	US-09-488-039A-829
117	78	5.6	292	2	US-09-540-236-3287	Sequence 3287, AP	190	74	5.3	282	2	US-09-583-110-3219
118	78	5.6	405	2	US-09-144-914-5	Sequence 5, App1	191	74	5.3	292	1	US-09-02-848-2
119	78	5.6	575	2	US-09-328-6465	Sequence 6465, AP	192	74	5.3	173	2	US-09-252-591A-2033
120	78	5.6	664	2	US-09-905-540-16458	Sequence 16458, AP	193	74	5.3	307	2	US-09-328-332-6226
121	77.5	5.6	238	2	US-09-328-352-7122	Sequence 7122, AP	194	74	5.3	332	2	US-09-902-540-13291
122	77.5	5.6	287	2	US-09-543-681A-5282	Sequence 5282, AP	195	74	5.3	407	2	US-09-303-518D-302
123	77.5	5.6	525	2	US-09-254-796A-27543	Sequence 27543, A	196	74	5.3	445	2	US-08-937-334-5
124	77.5	5.6	693	2	US-10-094-749-2517	Sequence 2517, AP	197	74	5.3	448	2	US-09-543-681A-7245
125	77.5	5.6	743	2	US-10-104-749-2340	Sequence 2340, AP	198	74	5.3	478	2	US-09-348-116-A-9619
126	77.5	5.6	126	2	US-09-328-6465	Sequence 6465, AP	199	74	5.3	727	2	US-09-543-681A-7968
127	77	5.5	318	2	US-09-711-279-3118	Sequence 3118, AP	200	74	5.3	900	2	US-09-134-001C-5655
128	77	5.5	385	2	US-09-540-236-3736	Sequence 3736, AP	201	74	5.3	937	2	US-09-490-039A-8466
129	77	5.5	506	2	US-09-715-919A-1	Sequence 1, App1	202	75	5.3	846	2	US-09-489-039A-8466
130	77	5.5	532	2	US-09-102-532A-7299	Sequence 7299, AP	203	75	5.3	360	1	US-08-597-336-11
131	77	5.5	397	2	US-09-328-7457	Sequence 7457, AP	204	75	5.3	360	1	US-08-746-632A-11
132	76.5	5.5	322	2	US-09-254-991A-32264	Sequence 32264, AP	205	75	5.3	391	1	US-08-721-178A-2
133	76.5	5.5	483	2	US-09-710-279-3132	Sequence 3132, AP	206	75	5.3	391	1	US-08-121-178A-2
134	76.5	5.5	568	2	US-09-940-016-6719	Sequence 6719, AP	207	75	5.3	416	2	US-08-103-454-5
135	76.5	5.5	596	2	US-09-94-016-8124	Sequence 8124, AP	208	75	5.3	391	1	US-08-461-690B-5
136	76.5	5.5	630	2	US-09-010-001C-4615	Sequence 4615, AP	209	75	5.3	391	1	US-08-101-003A-16
137	76.5	5.5	729	2	US-10-094-749-2118	Sequence 2118, AP	210	75	5.3	391	2	US-09-543-681A-8392
138	76	5.5	322	2	US-09-540-236-2364	Sequence 236, AP	211	75	5.3	395	2	US-09-275-252-A-13
139	76	5.5	361	2	US-09-482-273-236	Sequence 236, AP	212	75	5.3	416	2	US-09-543-681A-5655
140	76	5.5	378	2	US-09-105-532A-6501	Sequence 6501, AP	213	75	5.3	417	2	US-09-107-532A-4001
141	76	5.5	424	2	US-09-252-991A-18895	Sequence 18895, A	214	75	5.3	428	2	US-09-198-452A-720
142	76	5.5	429	2	US-09-922-501-10	Sequence 10, App1	215	75	5.3	428	2	US-09-438-185A-682
143	76	5.5	453	7	US-09-546-9-A-4893	Patent No. 5,684,633	216	75	5.3	514	2	US-09-489-039A-11902
144	76	5.5	633	2	US-09-252-991A-17394	Sequence 17394, A	217	75	5.3	564	2	US-09-902-510-16102
145	76	5.5	1155	2	US-09-944-016-10337	Sequence 10337, A	218	75	5.3	607	1	US-09-959-016-7108
146	75.5	5.4	313	2	US-09-252-991A-27133	Sequence 27133, A	219	75	5.3	630	1	US-09-543-681A-5655
147	75.5	5.4	401	2	US-09-489-039A-1156	Sequence 11546, A	220	75	5.3	630	1	US-09-107-532A-4001
148	75.5	5.4	445	2	US-09-328-352-6669	Sequence 6669, AP	221	75	5.3	630	1	US-09-107-532A-4001
149	75.5	5.4	517	2	US-09-248-796A-20437	Sequence 20437, A	222	75	5.3	717	2	US-09-134-000C-5833
150	75.5	5.4	453	2	US-09-854-122-49	Sequence 49, App1	223	75	5.3	1099	2	US-08-226-214-14
151	75.5	5.4	344	2	US-09-543-681A-6286	Sequence 6286, AP	224	75	5.3	2020	1	US-07-551-531-2
152	75.5	5.4	1172	2	US-09-328-352-6071	Sequence 6071, AP	225	75	5.3	2485	5	PCT-US94-00198-1
153	75	5.4	218	2	US-09-328-352-5215	Sequence 5215, AP	226	75	5.3	2485	5	PCT-US94-00198-1
154	75	5.4	399	2	US-09-107-433-3024	Sequence 9414, AP	227	75	5.3	630	1	US-09-543-681A-19167
155	75	5.4	290	2	US-09-134-001C-4893	Sequence 2024, AP	228	75	5.3	630	1	US-09-134-000C-5833
156	75	5.4	344	1	US-09-854-974-1	Sequence 1, App1	229	75	5.3	2818	2	US-07-366-039A-2
157	75	5.4	1155	2	US-09-543-681A-6286	Sequence 6286, AP	230	75	5.3	2818	2	US-09-543-681A-6286
158	75	5.4	394	2	US-09-144-9174-4	Sequence 4, App1	231	75	5.3	2818	2	US-09-328-352-7304
159	75	5.4	457	2	US-09-655-272-5	Sequence 50256, A	232	75	5.2	178	2	US-09-528-352-5593
160	75	5.4	579	2	US-09-248-796A-20256	Sequence 20256, A	233	75	5.2	187	2	US-09-134-001C-3355
161	75	5.4	408	2	US-09-720-317A-4	Sequence 4, App1	234	75	5.2	234	2	US-09-328-352-7918
162	75	5.4	420	2	US-09-255-368-6	Sequence 6, App1	235	75	5.2	291	2	US-09-252-991A-32938
163	75	5.4	1163	2	US-09-405-558-6	Sequence 6, App1	236	75	5.2	291	2	US-09-543-681A-32938
164	75	5.4	420	2	US-09-538-036-6	Sequence 6, App1	237	75	5.2	431	2	US-09-543-681A-32938
165	75	5.4	1172	2	US-09-489-039A-8037	Sequence 8037, AP	238	75	5.2	434	2	US-09-328-352-7304
166	75	5.4	524	2	US-09-248-796A-20256	Sequence 20256, A	239	75	5.2	445	1	US-09-90-108-148-2
167	75	5.4	579	2	US-09-720-317A-4	Sequence 4, App1	240	75	5.2	466	2	US-09-815-922-10
168	74.5	5.4	304	2	US-09-328-352-6459	Sequence 6, App1	241	75	5.2	3079	5	PCT-US94-00198-4
169	74.5	5.4	321	2	US-09-543-681A-31084	Sequence 31084, A	242	75	5.2	727	2	US-09-543-681A-32621
170	74.5	5.4	243	2	US-09-543-681A-5778	Sequence 5778, AP	243	75	5.2	281	2	US-09-540-236-2349
171	74.5	5.4	367	2	US-09-198-452A-1069	Sequence 1069, AP	244	75	5.2	319	2	US-09-543-681A-5338
172	74.5	5.4	367	2	US-09-438-185A-996	Sequence 996, AP	245	75	5.2	725	2	US-09-328-352-5055

246	413	5.2	US-09-540-236-3672	Sequence 3672, App	319	71	5.1	US-09-902-540-11956	Sequence 11956, A	
		5.2	US-09-449-1346	Sequence 1346, A	320	71	5.1	US-09-222-538A-37	Sequence 222, App	
		5.2	US-09-248-798A-20368	Sequence 20368, A	321	71	5.1	US-09-583-110-246	Sequence 2946, App	
		5.2	US-09-328-352-5096	Sequence 5096, App	322	71	5.1	US-09-107-333-3747	Sequence 3747, App	
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	250	72	5.2	US-09-328-352-5843	Sequence 13005, A	325	71	5.1	US-09-043-044-1	Sequence 1, App
	251	72	5.2	US-09-502-540-13005	Sequence 804, App	326	71	5.1	US-09-043-944-6	Sequence 6, App
	252	72	5.2	US-09-303-515D-804	Sequence 2, App	327	71	5.1	US-09-043-944-6	Sequence 1, App
	253	72	5.2	US-09-107-49D-2	Sequence 2981, App	328	71	5.1	US-10-811-199-6	Sequence 6, App
	254	72	5.2	US-09-134-001C-2981	Sequence 4671, App	329	71	5.1	US-09-279-1676	Sequence 1676, App
	255	72	5.2	US-09-543-688A-4671	Sequence 4, App	330	71	5.1	US-09-328-552-7117	Sequence 7117, App
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1003	4.6	US-09-518-959-8	Sequence 3546, Ap	1076	64	US-09-359-167-2
1004	4.6	US-09-54-681A-6388	Sequence 6388, Ap	1077	64	US-09-915-181A-7
1005	4.6	US-09-248-796A-152A-5	Sequence 15245, A	1078	64	US-09-328-522-6371
1006	4.6	US-10-114-270-144	Sequence 144, App	1079	64	US-09-605-703B-1200
1007	4.6	US-09-605-703B-1584	Sequence 1584, Ap	1080	64	US-09-902-540-12496
1008	4.6	US-09-905-540-11439	Sequence 11439, A	1081	64	PCT-US95-0923-2
1009	4.6	US-09-94-016-11434	Sequence 11109, A	1082	64	US-09-359-167-8
1010	4.6	US-07-902-546-2	Sequence 1, Appli	1083	64	US-09-107-532A-4163
1011	4.6	US-08-665-222B-6	Sequence 6, Appli	1084	64	US-09-549-016-7705
1012	4.6	US-08-24-41-2	Sequence 2, Appli	1085	64	US-09-605-703B-1200
1013	4.6	US-09-905-540-1025	Sequence 7025, Ap	1086	64	US-09-94-016-6935
1014	4.6	PCT-US91-09422-19	Sequence 19, Appli	1087	64	US-09-107-532A-6535
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1016	4.6	US-07-902-546-2	Sequence 8554, Ap	1089	64	US-09-107-532A-4163
1017	4.6	US-09-270-767-36480	Sequence 36480, A	1090	64	US-09-549-016-7705
1018	4.6	US-09-270-767-51697	Sequence 51697, A	1091	64	US-09-549-016-7705
1019	4.6	US-09-270-767-32080	Sequence 32080, A	1092	64	US-09-94-016-6935
1020	4.6	US-09-902-540-10737	Sequence 10737, A	1093	64	US-09-94-016-10311
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1022	4.6	US-09-542-236-2955	Sequence 2955, Ap	1095	64	US-09-542-23521-A
1023	4.6	US-09-247-155-89	Sequence 89, Appli	1096	64	US-09-552-991A-23521
1024	4.6	US-09-903-190-89	Sequence 89, Appli	1097	64	US-09-248-796A-20339
1025	4.6	US-09-543-681A-4487	Sequence 4487, Ap	1098	64	US-09-712-323-287
1026	4.6	US-09-328-352-4425	Sequence 4425, Ap	1099	64	US-09-949-016-10152
1027	4.6	US-09-107-532A-52991	Sequence 5290, Ap	1100	64	US-10-437-562A-46
1028	4.6	US-09-724-623-103	Sequence 103, Appli	1101	64	US-09-512-230C-32
1029	4.6	US-10-288-930-103	Sequence 103, Appli	1102	63.5	US-09-548-207A-363
1030	4.6	US-10-770-127-195	Sequence 195, App	1103	63.5	US-09-712-323-287
1031	4.6	US-10-770-127-33	Sequence 33, Appli	1104	63.5	US-09-462-136-2
1032	4.6	US-09-134-001C-3561	Sequence 3561, Appli	1105	63.5	US-09-949-016-10152
1033	4.6	US-08-671-978A-8	Sequence 8, Appli	1106	64	US-10-437-562A-21
1034	4.6	US-09-110-116-4	Sequence 4, Appli	1107	63.5	US-09-512-230C-32
1035	4.6	US-09-170-496D-164	Sequence 164, App	1108	63.5	US-09-548-207A-363
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1037	4.6	US-08-462-509B-4	Sequence 4, Appli	1110	63.5	US-09-462-136-2
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1039	4.6	US-09-328-352-7132	Sequence 7132, Ap	1112	63.5	US-09-462-046B-5
1040	4.6	US-08-462-509B-6	Sequence 6, Appli	1113	63.5	US-09-512-230C-32
1041	4.6	US-09-042-583-48	Sequence 48, Appli	1114	63.5	US-09-548-207A-363
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1043	4.6	US-09-914-098-58	Sequence 58, App	1116	63.5	US-09-462-046B-5
1044	4.6	PCT-US95-05616-4	Sequence 6, Appli	1117	63.5	US-09-489-039A-8478
1045	4.6	US-09-107-532A-52990	Sequence 5290, Ap	1118	63.5	US-09-4399-A
1046	4.6	US-09-110-116-4	Sequence 4, Appli	1119	63.5	US-09-512-230C-32
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1123	4.6	328	2	US-09-489-039A-13029	Sequence 29029, A	US-08-621-493-4	4.5	253	1	US-08-621-493-4
1124	4.6	332	2	US-09-252-991A-31791	Sequence 31791, A	US-08-621-493-4	4.5	253	2	US-09-260-123-4
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1126	4.6	332	2	US-09-980-145-37	Sequence 37, App1	US-09-260-123-4	4.5	253	2	US-09-260-123-4
1127	4.6	341	2	US-10-094-749-2185	Sequence 2185, App1	US-09-260-123-4	4.5	259	2	US-09-268-312-6237
1128	4.6	345	2	US-09-248-796A-20780	Sequence 20780, A	US-09-260-123-4	4.5	259	2	US-09-260-123-4
1129	4.6	356	2	US-08-567-882-7	Sequence 7, App1	US-09-260-123-4	4.5	273	2	US-09-493-016-8333
1130	4.6	359	2	US-09-248-796A-17633	Sequence 17633, A	US-09-260-123-4	4.5	279	2	US-09-489-019A-13333
1131	4.6	378	2	US-09-540-236-3528	Sequence 3528, App1	US-09-260-123-4	4.5	284	2	US-09-270-767-31635
1132	4.6	379	1	US-08-221-108-18	Sequence 18, App1	US-09-260-123-4	4.5	284	2	US-09-270-767-48852
1133	4.6	379	1	US-09-073-674-18	Sequence 18, App1	US-09-260-123-4	4.5	287	2	US-09-134-000C-594
1134	4.6	391	1	US-09-489-039A-9791	Sequence 9791, App1	US-09-260-123-4	4.5	289	2	US-09-260-123-4
1135	4.6	404	1	US-08-428-423-7	Sequence 7, App1	US-09-260-123-4	4.5	290	2	US-09-910-174B-8
1136	4.6	404	5	PCT-US93-10301-7	Sequence 7, App1	US-09-260-123-4	4.5	290	2	US-09-910-174B-8
1137	4.6	405	2	US-09-248-796A-179655	Sequence 17965, A	US-09-260-123-4	4.5	290	2	US-09-260-123-4
1138	4.6	414	2	US-09-489-039A-10869	Sequence 10869, A	US-09-260-123-4	4.5	290	2	US-09-260-123-4
1139	4.6	430	2	US-09-583-110-4230	Sequence 4230, App1	US-09-260-123-4	4.5	290	2	US-09-645-089-4
1140	4.6	430	2	US-09-248-796A-14556	Sequence 14556, A	US-09-260-123-4	4.5	290	2	US-09-645-089-4
1141	4.6	437	2	US-09-107-433-3678	Sequence 3678, App1	US-09-260-123-4	4.5	290	2	US-09-645-089-4
1142	4.6	449	2	US-09-949-016-8594	Sequence 8594, App1	US-09-260-123-4	4.5	290	3	US-10-115-603-4
1143	4.6	457	2	US-09-721-870-26	Sequence 26, App1	US-09-260-123-4	4.5	299	2	US-09-583-110-2991
1144	4.6	458	2	US-09-328-352-5083	Sequence 5083, App1	US-09-260-123-4	4.5	345	2	US-09-362-123A-2
1145	4.6	470	2	US-09-554-681A-4625	Sequence 4625, App1	US-09-260-123-4	4.5	345	2	US-09-107-532A-4426
1146	4.6	473	1	US-08-439-131A-4	Sequence 4, App1	US-09-260-123-4	4.5	345	2	US-09-107-532A-4426
1147	4.6	473	1	US-08-440-674-3	Sequence 3, App1	US-09-260-123-4	4.5	345	2	US-09-199-181-2
1148	4.6	473	2	US-08-870-337-7	Sequence 7, App1	US-09-260-123-4	4.5	345	2	US-09-199-181-2
1149	4.6	473	2	US-09-303-518D-378	Sequence 378, App1	US-09-260-123-4	4.5	345	2	US-09-199-181-2
1150	4.6	476	2	US-09-489-039A-10203	Sequence 10203, A	US-09-260-123-4	4.5	345	2	US-09-199-181-2
1151	4.6	482	2	US-09-328-352-7784	Sequence 7784, App1	US-09-260-123-4	4.5	345	3	US-09-989-726-2
1152	4.6	488	1	US-08-115-365-2	Sequence 2, App1	US-09-260-123-4	4.5	345	3	US-09-989-514-2
1153	4.6	488	1	US-08-586-897-2	Sequence 2, App1	US-09-260-123-4	4.5	345	3	US-09-989-514-2
1154	4.6	488	2	US-09-826-509-61	Sequence 561, App1	US-09-260-123-4	4.5	345	3	US-09-989-514-2
1155	4.6	521	2	US-08-956-322-4	Sequence 4, App1	US-09-260-123-4	4.5	345	3	US-09-989-514-2
1156	4.6	521	2	US-08-489-039A-9781	Sequence 9781, App1	US-09-260-123-4	4.5	345	3	US-09-989-514-2
1157	4.6	531	2	US-09-710-279-920	Sequence 920, App1	US-09-260-123-4	4.5	346	2	US-09-149-476-493
1158	4.6	534	2	US-09-830-123-2	Sequence 2, App1	US-09-260-123-4	4.5	350	2	US-09-202-540-1418
1159	4.6	542	2	US-09-902-540-12884	Sequence 2, App1	US-09-260-123-4	4.5	354	2	US-09-202-567-54287
1160	4.6	557	2	US-09-248-796A-20375	Sequence 20375, A	US-09-260-123-4	4.5	361	2	US-09-543-681A-5180
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1162	4.6	600	2	US-08-800-291B-4	Sequence 4, App1	US-09-260-123-4	4.5	365	1	US-08-333-610-7
1163	4.6	650	2	US-09-110-116-1	Sequence 1, App1	US-09-260-123-4	4.5	365	2	US-09-377-452-7
1164	4.6	652	2	US-08-956-322-2	Sequence 2, App1	US-09-260-123-4	4.5	374	2	US-09-721-341-8
1165	4.6	652	2	US-09-492-709A-352	Sequence 352, App1	US-09-260-123-4	4.5	374	2	US-09-721-341-8
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1168	4.6	685	2	US-09-248-796A-15264	Sequence 685, App1	US-09-260-123-4	4.5	387	2	US-09-549-848B-17
1169	4.6	716	2	US-09-303-518D-106	Sequence 106, App1	US-09-260-123-4	4.5	391	2	US-09-588-033A-17
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1172	4.6	799	2	US-10-104-047-2335	Sequence 2335, App1	US-09-260-123-4	4.5	409	2	US-09-605-703B-2146
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1176	4.6	923	2	US-09-397-885-1	Sequence 1, App1	US-09-260-123-4	4.5	430	2	US-09-443-041A-18
1177	4.6	923	2	US-09-969-362-1	Sequence 2335, App1	US-09-260-123-4	4.5	430	2	US-09-134-000C-4627
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1179	4.6	1007	2	US-09-221-059-28	Sequence 28, App1	US-09-260-123-4	4.5	438	1	US-08-677-049-9
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1181	4.6	1098	2	US-08-726-214-10	Sequence 10, App1	US-09-260-123-4	4.5	443	2	US-09-16-510-6
1182	4.6	1895	1	US-08-619-554-4	Sequence 4, App1	US-09-260-123-4	4.5	443	2	US-09-004-343-6
1183	4.6	1895	2	US-08-487-558B-136	Sequence 13, App1	US-09-260-123-4	4.5	443	2	US-09-330A-33
1184	4.6	2522	2	US-08-251-645-13	Sequence 13, App1	US-09-260-123-4	4.5	461	1	US-08-194-338-4
1185	4.6	219	1	US-08-186-529-4	Sequence 4, App1	US-09-260-123-4	4.5	461	1	US-08-194-338-4
1186	4.6	219	1	US-08-489-386A-4	Sequence 4479, App1	US-09-260-123-4	4.5	478	2	US-09-107-532A-6105
1187	4.6	154	2	US-08-248-796A-20059	Sequence 20059, A	US-09-260-123-4	4.5	478	2	US-09-149-016-6543
1188	4.6	175	2	US-09-543-681A-8328	Sequence 8328, App1	US-09-260-123-4	4.5	485	2	US-09-949-016-10455
1189	4.6	214	2	US-09-107-532A-5408	Sequence 5408, App1	US-09-260-123-4	4.5	497	2	US-09-248-796A-20395
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1193	4.6	250	2	US-09-107-532A-6270	Sequence 6270, App1	US-09-260-123-4	4.5	580	2	US-09-657-255-2
1194	4.6	253	1	US-09-265-087-4	Sequence 4, App1	US-09-260-123-4	4.5	597	2	US-09-328-352-4703

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	683	US-08-979-847B-210	Sequence 39, Appli	1345	4.5	292	2	Sequence 7918, AP
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	63	US-10-166-719A-58	Sequence 17, Appli	1348	4.5	294	2	US-09-328-352-709B
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	63	US-08-702-229-17	Sequence 18, Appli	1350	4.5	324	2	Sequence 5947, AP
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	1276	US-09-313-942-24	Sequence 24, Appli	1351	4.5	326	2	Sequence 8980, AP
	63	US-10-301-661B-18	Sequence 7, Appli	1351	4.5	326	2	US-09-252-991A-18980
	1277	US-09-795-927-7	Sequence 7, Appli	1352	4.5	326	2	Sequence 31150, A
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	63	US-10-208-059-14	Sequence 14, Appli	1354	4.5	351	2	Sequence 112523, A
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	63	US-10-135-988-4	Sequence 4, Appli	1359	4.5	361	2	Sequence 19, Appli
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	63	US-10-135-988-4	Sequence 6, Appli	1361	4.5	371	2	Sequence 112523, A
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	1288	US-09-653-499-4	Sequence 6, Appli	1368	4.5	373	2	Sequence 7048, AP
	63	US-09-653-499-4	Sequence 6, Appli	1369	4.5	376	2	Sequence 7545, AP
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	63	US-10-135-988-4	Sequence 6, Appli	1371	4.5	382	2	Sequence 32165, A
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	63	US-10-135-988-4	Sequence 6, Appli	1373	4.5	398	2	Sequence 61326, AP
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; Patent No. 6930170
; GENERAL INFORMATION:
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; APPLICANT: Zhang, Zemin
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; PRIOR APPLICATION NUMBER: 60/090690
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
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; PRIOR APPLICATION NUMBER: 60/091519

; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 1392; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 266; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MWFFQGLSFLPSALVIVTSAFISYITAVTLHHIDPALPYISDTGTVAPEKCFGAML 60
Db      1 MWFFQGLSFLPSALVIVTSAFISYITAVTLHHIDPALPYISDTGTVAPEKCFGAML 60
Qy      61 NIAAVIATIAYVRKVQHALSPEENVIKLINKAGLVLGILSCLGLSIVANFOQTTLFAA 120
Db      61 NIAAVIATIAYVRKVQHALSPEENVIKLINKAGLVLGILSCLGLSIVANFOQTTLFAA 120
Qy      121 HVSGAVLTFCMGSLNMVFQTLISYQMPKTHGKQFYEWIRLILWVGVSALSMLTCSSVL 180
Db      121 HVSGAVLTFCMGSLNMVFQTLISYQMPKTHGKQFYEWIRLILWVGVSALSMLTCSSVL 180
Db      181 HSGNFGTDLEQLHNPEDKGYVLMIMTTAEWSMSFSFFGFLYIRDFOKISRVEAN 240
Db      181 HSGNFGTDLEQLHNPEDKGYVLMIMTTAEWSMSFSFFGFLYIRDFOKISRVEAN 240
Qy      241 LHGLTYDTPCPINNERTLLSRDI 266
Db      241 LHGLTYDTPCPINNERTLLSRDI 266

RESULT 3
US-09-997-333-23
; Sequence 23, Application US/09997333
; Patent No. 6933836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi Avi J.
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein David
; APPLICANT: Desnoyers Luc
; APPLICANT: Eaton Dan L.
; APPLICANT: Ferrara Napoleone
; APPLICANT: Fong Sherman
; APPLICANT: Gerber Hanspeter
; APPLICANT: Gerritsen Mary E.
; APPLICANT: Goddard Audrey
; APPLICANT: Godowski Paul J.
; APPLICANT: Grimaldi J Christopher
; APPLICANT: Gurney Austin L.
; APPLICANT: Kliaviv Ivar J.
; APPLICANT: Napier Mary A.
; APPLICANT: Pan James
; APPLICANT: Paoni Nicholas F.
; APPLICANT: Roy Margaret Ann
; APPLICANT: Stewart Timothy A.
; APPLICANT: Tumas Daniel
; APPLICANT: Watanabe Colin K.
; APPLICANT: Williams P. Mickey
; APPLICANT: Wood William I.
; APPLICANT: Zheni
; TITLE OF INVENTION: Secret and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

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; PRIORITY APPLICATION NUMBER: 60/062250
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; PRIORITY FILING DATE: 1998-06-12
; PRIORITY APPLICATION NUMBER: 60/089440

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PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
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 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match Score: 100.0%; Score: 1392; DB: 2; Length: 266;
 Best Local Similarity: 100.0%; Pred. No.: 1.2e-14;
 Matches: 266; Conservative: 0; Mismatches: 0; Gaps: 0;

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1	1	MWWFQQGSLFLPSALVWTSAAIFPSYTAVTLLHIDPALPTISDTAVPKCLFGAML	60
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Qy	61	NIAAVLCLATIVYRYKQHALSPENNTIKLNKAGLVIGILSCLGLSTIVANFQKTLFAA	120
Qy	61	NIAAVLCLATIVYRYKQHALSPENNTIKLNKAGLVIGILSCLGLSTIVANFQKTLFAA	120
Qy	121	HVSGAVLTTGCGSLYMFVOTILSYQMQPKIHGKQVFWRLLYIWCGVMSMLTCSSVL	180
Do	121	HVSGAVLTTGCGSLYMFVOTILSYQMQPKIHGKQVFWRLLYIWCGVMSMLTCSSVL	180
Qy	181	HSGNFGTDLIBQKLHWNPDKGYVLUHMTTAAEWSMSFFFGFLTYIRDFOQKISLRVEAN	240
Do	181	HSGNFGTDLIBQKLHWNPDKGYVLUHMTTAAEWSMSFFFGFLTYIRDFOQKISLRVEAN	240
Qy	241	LHGGLTLYDTPACPINNETRLLSRDI	266
Db	241	LHGGLTLYDTPACPINNETRLLSRDI	266

RESULT 4
 US-09-932-598-23
 Sequence 23, Application US/0992598

GENERAL INFORMATION:

- APPLICANT: Ashkenazi, Avi J.
- APPLICANT: Baker, Kevin P.
- APPLICANT: Bostein, David
- APPLICANT: Desnoyers, Luc
- APPLICANT: Eaton, Dan L.
- APPLICANT: Ferrara, Napoleone
- APPLICANT: Fong, Sherman
- APPLICANT: Gerber, Hanspeter
- APPLICANT: Gerritsen, Mary E.
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul J.
- APPLICANT: Grimaldi, J. Christopher
- APPLICANT: Gurney, Austin L.
- APPLICANT: Kijavin, Ivar J.
- APPLICANT: Napier, Mary A.
- APPLICANT: Pan, James
- APPLICANT: Paoni, Nicholas F.
- APPLICANT: Roy, Margaret Ann
- APPLICANT: Stewart, Timothy A.
- APPLICANT: Tumas, Daniel
- APPLICANT: Watanabe, Colin K.
- APPLICANT: Williams, P. Mickey

APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P230PIC61
 CURRENT APPLICATION NUMBER: US/09/989,735
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match Score 1392; DB 2; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;
 Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNWFOQGISELPSALVWTSAAIFSYTAVTLLHIDPALPVISDTGVAPEKCLFGAML 60
 Db 1 MNWFOQGISELPSALVWTSAAIFSYTAVTLLHIDPALPVISDTGVAPEKCLFGAML 60
 Qy 61 NIAAVLCAATTIVRYKQWHALSPEENVILKLNAGLVIGLSCLGLSVANFQKTLFAA 120
 Db 61 NIAAVLCAATTIVRYKQWHALSPEENVILKLNAGLVIGLSCLGLSVANFQKTLFAA 120
 Qy 121 HSGAVLTFGMSLYMFQTLISYQMKIHKQVFWRLLIVWCGSALSMLTC5SVL 180
 Db 121 HSGAVLTFGMSLYMFQTLISYQMKIHKQVFWRLLIVWCGSALSMLTC5SVL 180
 Qy 181 HSGNFGTDLBOKLHNPDKGYVLMITTAAEAMSMSFRGGFLTYIRDQKISLRVEAN 240
 Db 181 HSGNFGTDLBOKLHNPDKGYVLMITTAAEAMSMSFRGGFLTYIRDQKISLRVEAN 240
 Qy 241 LHGILTYDAPCPINNEETRLSRDI 266
 Db 241 LHGILTYDAPCPINNEETRLSRDI 266

RESULT 6
 US-09-389-726-23
 ; Sequence No. 7018811
 ; Patent No. 7018811
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton,Dan L.
 APPLICANT: Ferrara,Napoleone
 APPLICANT: Fong,Sherman
 APPLICANT: Gerber,Hanspeter
 APPLICANT: Gerritsen,Mary E.
 APPLICANT: Goddard,Audrey
 APPLICANT: Godowski,Paul J.
 APPLICANT: Grimaldi,J.Christopher
 APPLICANT: Gurney,Austin L.
 APPLICANT: Klijavin,Ivar J.
 APPLICANT: Napier,Mary A.
 APPLICANT: Pan,James
 APPLICANT: Paoni,Nicholas F.
 APPLICANT: Roy,Margaret Ann
 APPLICANT: Stewart,Timothy A.
 APPLICANT: Tumas,Daniel
 APPLICANT: Watansabe,Colin K.
 APPLICANT: Williams,P.Mickey
 APPLICANT: Wood,William I.
 APPLICANT: Zhang,Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730PLIC0
 CURRENT APPLICATION NUMBER: US/09/989,726
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444

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Query Match 100.0% ; Score 1392; DB 3; Length 266;

Best Local Similarity	Pred.	No. 1..2e-144;	Mismatches	Indels	Gaps	O;
Matches 266;	Conservative	0;		0;		

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Db 1 MWFFQQSLFPLSAVLTWAAFIIFSVITAVTLHIDPALPYISDGTVAPEKCLFGAML 60

Qy 61 NIAAVLCIATIVRKQYHALSPEENVIKUNKAGLVIGLISCLGLSIVANFQKTTILFAA 120
Db 61 NIAAVLCIATIVRKQYHALSPEENVIKUNKAGLVIGLISCLGLSIVANFQKTTILFAA 120

Qy 121 HVSGAVLTFGMSSLYMEVQTLISYQMPKIHGROVFLRLIIVWCGVSALSMLTCSSVL 180
Db 121 HVSGAVLTFGMSSLYMEVQTLISYQMPKIHGQVFLRLIIVWCGVSALSMLTCSSVL 180

Qy 181 HSGNFGTDLBQLHNPEDKGTVLHMITAEMSFSFGFLTYIRDQKISLRVEAN 240
Db 181 HSGNFGTDLBQLHNPEDKGTVLHMITAEMSFSFGFLTYIRDQKISLRVEAN 240

Qy 241 LMCLTLYDTAPCPINNERTLRSRDI 266
Db 241 LMCLTLYDTAPCPINNERTLRSRDI 266

RESULT 7
 US-09-997-514-23
 Sequence 23, Application US/09997514
 Patent No. 7019116

GENERAL INFORMATION

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kjavir, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P230PIC46

CURRENT APPLICATION NUMBER: US/09/997-514

PRIOR FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/0499787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/0833322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

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PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/088025

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PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088029

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088030

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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;
 Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MWFFQQGSLPLPSALVIVNTSAATFSYTTAVLHIDALPYISDTGTVAPEKCLFGML 60

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 Db 61 NIAAVLCAIATIVRYKQWHALSPEENVTKLNKAGLVGILSCLGLSVANFORTLFAA 120

Qy 121 HVSGAVLTFGMGLMFMVOTLSTOMQPKHGVFWRLLVTWCGTVALSMLTCSSVL 180
 Db 121 HVSGAVLTFGMGLMFMVOTLSTOMQPKHGVFWRLLVTWCGTVALSMLTCSSVL 180

RESULT 8
 US-09-989-728-23
 Sequence 23 Application US/09989728
 Patent No. 7029873
 GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Baton, Dan L.
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gerber, Hanspetter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Klijavin, Ivar J.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Watanabe, Colin K.
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
 / APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 Acids Encoding the Same
 FILE REFERENCE: P2730PLC72
 CURRENT APPLICATION NUMBER: US/09/989,728
 CURRENT FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952

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Query Match      100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1. 2e-144;
Matches 266; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
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 Db 181 HSGNFGTLEQKLHWNPPDKGYVLHMITTAEWMSMSEFFGPFLTVIRDFQKISLRVEAN 240
 Qy 241 LHGLTYDTPAPCPINNETRLRSID 266
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RESULT 9
 ; Sequence 23, Application US/09997349
 ; Patent No. 7034106
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Klijvin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Michael
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730P1C37
 ; CURRENT APPLICATION NUMBER: US/09/997,149
 ; CURRENT FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
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 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
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 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 60/078910
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 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182

; PRIOR FILING DATE: 1998-07-09
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RESULT 10
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 Patent No. 7034122
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerriksen, Mary B.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Klijavins, Irvar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; ACIDS Encoding the Same
 ; FILE REFERENCE: P2730PIC3B
 ; CURRENT APPLICATION NUMBER: US/09/997,653
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
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 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25

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 PRIOR FILING DATE: 1998-07-07
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match Score 1392; DB 3; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;
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 Db 61 NIAAVLCAIATIYRYKQVHALSPENVVIKLNAKGLVQGILSCLGSLSTVANFQKTLFAA 120

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 Db 241 LHGTLYDTAPCPINNETRRLSRDI 266

RESULT 11
 US-09-293A-23
 ; Sequence 23, Application US/0988293A

GENERAL INFORMATION:
 APPLICANT: Abkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goodard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2730P1C56
 CURRENT APPLICATION NUMBER: US/09/989,293A
 CURRENT FILING DATE: 2001-11-20
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 LHGLTLYDTACPINNERTLRSIDI 266
Db 241 LHGLTLYDTACPINNERTLRSIDI 266

RESULT 12
US-09-663-600A-190
; Sequence 190, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Ducleurt, Aymeric
; APPLICANT: Bougueret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31-US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pn

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SEQ ID NO 190
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 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: SIGNAL
 NAME/KEY: SIGNAL
 LOCATION: -21..-1
 US-09-663-600A-190

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 ; Patent No. 6380362

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RESULT 1.5
 US-09-663-600A-96
 ; Sequence 96, Application US/09663600A
 ; Patent No. 6572068

GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, Jean-Baptiste
 APPLICANT: Bouqueret, Lydie
 TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
 FILE REFERENCE: 31.US3.CIP
 CURRENT APPLICATION NUMBER: US/09/663,600A
 CURRENT FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: 09/191,997
 PRIOR FILING DATE: 1998-11-13
 PRIOR APPLICATION NUMBER: 60/066,677
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/069,957
 PRIOR FILING DATE: 1997-12-17
 PRIOR APPLICATION NUMBER: 60/074,121
 PRIOR FILING DATE: 1998-02-09
 PRIOR APPLICATION NUMBER: 60/081,563
 PRIOR FILING DATE: 1998-04-13
 PRIOR APPLICATION NUMBER: 60/096,116
 PRIOR FILING DATE: 1998-08-10
 PRIOR APPLICATION NUMBER: 60/099,273
 PRIOR FILING DATE: 1998-09-04
 NUMBER OF SEQ ID NOS: 229
 SOFTWARE: Patent-pm
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 FEATURE: SIGNAL
 NAME/KEY: SIGNAL
 LOCATION: -21..-1
 US-09-663-600A-96

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RESULT 1.5
 US-09-724-864-38
 ; Sequence 38, Application US/09724864
 ; Patent No. 6380362

GENERAL INFORMATION:
 APPLICANT: Murison, James G.
 TITLE OF INVENTION: Polynucleotides, polypeptides expressed by the polynucleotides and methods for their use.

FILE REFERENCE: 11000-10500U
 CURRENT APPLICATION NUMBER: US/09/724,864
 CURRENT FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
 PRIOR FILING DATE: 1999-12-23
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 TYPE: PRT
 ORGANISM: Mouse

RESULT 1.5
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 ; Sequence 130, Application US/09663600A
 ; Patent No. 6572068

GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, Jean-Baptiste
 APPLICANT: Bouqueret, Lydie
 TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
 FILE REFERENCE: 31.US3.CIP
 CURRENT APPLICATION NUMBER: US/09/663,600A
 CURRENT FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: 09/191,997
 PRIOR FILING DATE: 1998-11-13
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 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/069,957
 PRIOR FILING DATE: 1997-12-17
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 PRIOR FILING DATE: 1998-02-09
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 PRIOR FILING DATE: 1998-04-13
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 PRIOR FILING DATE: 1998-08-10
 PRIOR APPLICATION NUMBER: 60/099,273
 PRIOR FILING DATE: 1998-09-04
 NUMBER OF SEQ ID NOS: 229
 SOFTWARE: Patent-pm

RESULT 1.5
 US-09-663-600A-130
 ; Sequence 130, Application US/09663600A
 ; Patent No. 6572068

GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, Jean-Baptiste
 APPLICANT: Bouqueret, Lydie
 TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
 FILE REFERENCE: 31.US3.CIP
 CURRENT APPLICATION NUMBER: US/09/663,600A

/* CURRENT FILING DATE: 2000-09-15
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Search completed: August 28, 2006, 17:43:02
Job time : 69 secs

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GenCore version 5.1.9

OM protein - protein search, using SW model

Run on: August 28, 2006, 17:37:50 ; Search time 34 Seconds

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5	151.5	10.9	437	7 US-11-395-249-66	Sequence 66, Appl
6	93.9	7.1	187	7 US-11-299-697-4787	Sequence 4787, Appl
7	93.5	6.7	303	7 US-11-056-8358B-83608	Sequence 83608, Appl
8	93.5	6.7	379	7 US-11-056-355B-83607	Sequence 83607, Appl
9	88	6.3	312	7 US-11-056-355B-4953	Sequence 4953, Appl
10	88	6.3	313	7 US-11-299-4952	Sequence 4952, Appl
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12	88	6.3	932	6 US-10-449-902-55200	Sequence 55200, Appl
13	87.5	6.3	482	7 US-11-330-403-16766	Sequence 16766, Appl
14	85.5	6.2	372	6 US-10-471-571A-4918	Sequence 4918, Appl
15	85.5	6.1	481	7 US-11-178-538-37	Sequence 37, Appl
16	85.5	6.1	545	6 US-11-399-249-26	Sequence 26, Appl
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74	78.5	5.6	793	7 US-11-325-276-15	Sequence 62, Appl
75	78	5.6	309	7 US-11-178-538-55	Sequence 55, Appl
76	78	5.6	309	7 US-11-1367-182-15	Sequence 15, Appl
77	78	5.6	309	7 US-11-178-538-62	Sequence 62, Appl
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81	78	5.6	355	6 US-11-056-355B-539892	Sequence 539892, Appl
82	78	5.6	362	6 US-10-953-349-14108	Sequence 14108, Appl
83	78	5.6	362	7 US-11-056-355B-53891	Sequence 53891, Appl
84	77.5	5.6	288	7 US-11-130-403-9006	Sequence 9006, Appl
85	77.5	5.6	316	6 US-10-449-902-55440	Sequence 55440, Appl
86	77.5	5.6	392	7 US-11-056-355B-41822	Sequence 41822, Appl
87	77.5	5.6	394	7 US-11-056-355B-41821	Sequence 41821, Appl
88	77.5	5.6	396	6 US-10-449-902-51643	Sequence 51643, Appl
89	77.5	5.6	445	7 US-11-056-355B-44865	Sequence 44865, Appl
90	77.5	5.6	473	7 US-11-056-355B-70692	Sequence 70692, Appl
91	77.5	5.6	480	7 US-11-056-355B-70691	Sequence 70691, Appl
92	77.5	5.6	491	7 US-11-056-355B-30245	Sequence 30245, Appl
93	77.5	5.6	498	7 US-11-056-355B-80244	Sequence 80244, Appl
94	77.5	5.6	498	7 US-11-056-355B-80244	Sequence 80244, Appl
95	77.5	5.6	526	7 US-11-056-355B-70690	Sequence 70690, Appl
96	77.5	5.6	526	7 US-11-056-355B-80243	Sequence 80243, Appl
97	77.5	5.6	635	7 US-11-056-355B-44864	Sequence 44864, Appl
98	77.5	5.6	635	7 US-10-449-902-49559	Sequence 49559, Appl

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107	75	5.4	282	7	US-11-056-355B-73048	Sequence 73048, A	Sequence 3, Appl
108	75	5.4	439	7	US-11-342-731-4	Sequence 4, Appl	Sequence 17517, A
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112	75	5.4	500	7	US-11-190-750-140	Sequence 140, App	Sequence 17515, A
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121	74	5.4	345	7	US-11-056-355B-41823	Sequence 41823, A	Sequence 42805, A
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129	74	5.3	383	6	US-10-953-349-5125	Sequence 5125, Ap	Sequence 50526, A
130	74	5.3	385	6	US-10-449-902-49336	Sequence 49336, A	Sequence 50526, A
131	74	5.3	404	7	US-11-330-403-45922	Sequence 4592, Ap	Sequence 41514, A
132	74	5.3	409	6	US-10-953-349-5124	Sequence 5124, Ap	Sequence 356, App
133	74	5.3	532	6	US-10-953-349-5123	Sequence 5123, Ap	Sequence 118, App
134	74	5.3	979	6	US-10-449-902-41275	Sequence 41275, A	Sequence 118, App
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137	73	5.3	366	7	US-11-056-355B-92113	Sequence 92113, A	Sequence 16813, A
138	73	5.3	370	7	US-11-056-355B-88156	Sequence 88156, A	Sequence 89701, A
139	73	5.3	979	6	US-10-449-902-41275	Sequence 92112, A	Sequence 93457, A
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141	73	5.3	384	7	US-11-056-355B-92111	Sequence 92111, A	Sequence 6882, Ap
142	73	5.3	441	7	US-11-330-438-18115	Sequence 18115, A	Sequence 5276, Ap
143	73	5.3	494	7	US-11-056-355B-91629	Sequence 91629, A	Sequence 14572, A
144	73	5.3	494	7	US-11-056-355B-95355	Sequence 95385, A	Sequence 87219, A
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153	73	5.2	332	6	US-10-953-349-22929	Sequence 22929, A	Sequence 46754, A
154	73	5.2	365	6	US-10-449-902-51917	Sequence 54621, A	Sequence 6, Appl
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157	73	5.2	523	7	US-11-056-355B-72614	Sequence 72694, A	Sequence 7378, Ap
158	73	5.2	355	6	US-10-953-349-22927	Sequence 22927, A	Sequence 9179, Ap
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161	73	5.2	401	7	US-11-216-529-3	Sequence 234, A	Sequence 9711, Ap
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163	73	5.2	458	7	US-11-056-355B-13955	Sequence 13955, A	Sequence 94055, A
164	73	5.2	458	7	US-11-056-355B-18220	Sequence 18291, A	Sequence 46126, A
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167	72	5.2	290	7	US-11-056-355B-69798	Sequence 52748, A	Sequence 7065, A
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171	72	5.2	423	6	US-10-953-349-16496	Sequence 16496, A	Sequence 9711, Ap

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266	70.5	546	7	US-11-056-3555B-87887	Sequence 87887, A	69.5	5.0	US-11-056-3555B-87887
267	70.5	553	6	US-10-517-552-10	Sequence 10, Appli	69.5	5.0	US-10-517-552-10
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270	70.5	619	7	US-11-318-947-46	Sequence 46, Appli	69.5	5.0	US-11-318-947-46
271	70.5	687	7	US-11-341-947-42	Sequence 2, Appli	69.5	5.0	US-11-341-947-42
272	70.5	687	7	US-11-218-716-10	Sequence 10, Appli	69.5	5.0	US-11-218-716-10
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282	70.5	1058	7	US-11-056-3555B-11256	Sequence 11256, A	69.5	5.0	US-11-056-3555B-11256
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290	70.5	218	7	US-11-056-3555B-102110	Sequence 102310, A	69.5	5.0	US-11-056-3555B-102110
291	70.5	218	7	US-11-056-3555B-112549	Sequence 113549, A	69.5	5.0	US-11-056-3555B-112549
292	70.5	364	6	US-10-449-902-31380	Sequence 31380, A	69.5	5.0	US-10-449-902-31380
293	70.5	905	6	US-10-449-902-51444	Sequence 49967, A	69.5	5.0	US-10-449-902-51444
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296	70.5	288	7	US-11-330-403-8004	Sequence 7169, AP	69.5	5.0	US-11-330-403-8004
297	70.5	296	7	US-10-449-902-2246	Sequence 2246, AP	69.5	5.0	US-10-449-902-2246
298	70.5	364	6	US-10-449-902-43438	Sequence 43438, A	69.5	5.0	US-10-449-902-43438
299	70.5	202	6	US-10-449-902-51445	Sequence 21445, A	69.5	5.0	US-10-449-902-51445
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306	69.5	502	7	US-11-056-3555B-27404	Sequence 27404, A	69.5	5.0	US-11-056-3555B-27404
307	69.5	502	7	US-11-056-3555B-101409	Sequence 74656, A	69.5	5.0	US-11-056-3555B-101409
308	69.5	226	7	US-11-056-3555B-11249	Sequence 112649, A	69.5	5.0	US-11-056-3555B-11249
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395	68.5	4.9	956	7	US-11-056-355B-91294	Sequence 91294, A	Sequence 53776, A
396	68.5	4.9	956	7	US-11-056-355B-95505	Sequence 95050, A	Sequence 31, App1
397	68.5	4.9	967	7	US-11-056-355B-100335	Sequence 100335,	Sequence 5118, AP
398	68.5	4.9	967	7	US-11-056-355B-111574	Sequence 111574,	Sequence 40088, A
399	68.5	4.9	1066	7	US-11-056-355B-75745	Sequence 75745, A	Sequence 5154, AP
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404	68.5	4.9	1084	7	US-11-056-355B-100334	Sequence 100334,	Sequence 6208, AP
405	68.5	4.9	1084	7	US-11-056-355B-111573	Sequence 111573,	Sequence 6208, AP
406	68.5	4.9	1084	7	US-11-056-325-276-24	Sequence 24, App1	Sequence 6208, AP
407	68	4.9	217	7	US-11-056-355B-73050	Sequence 73050, A	Sequence 6208, AP
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411	68	4.9	305	6	US-10-471-571A-2352	Sequence 2352, AP	Sequence 6208, AP
412	68	4.9	355	7	US-11-056-355B-7888	Sequence 475, APP	Sequence 6208, AP
413	68	4.9	369	7	US-11-056-355B-7888	Sequence 7888, A	Sequence 6208, AP
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417	68	4.9	443	7	US-11-056-355B-111478	Sequence 111478,	Sequence 6208, AP
418	68	4.9	457	7	US-11-310-403-927	Sequence 927, APP	Sequence 6208, AP
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421	68	4.9	458	7	US-11-311-789A-438	Sequence 438, APP	Sequence 6208, AP
422	68	4.9	461	7	US-11-334-403-10255	Sequence 10235, A	Sequence 6208, AP
423	68	4.9	461	7	US-11-056-355B-111478	Sequence 111478,	Sequence 6208, AP
424	68	4.9	461	7	US-11-310-403-927	Sequence 927, APP	Sequence 6208, AP
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427	68	4.9	493	7	US-11-330-403-7774	Sequence 7774, APP	Sequence 6208, AP
428	68	4.9	506	7	US-11-056-355B-100238	Sequence 100238,	Sequence 6208, AP
429	68	4.9	506	7	US-10-449-902-4419	Sequence 111477, A	Sequence 6208, AP
430	68	4.9	510	6	US-11-310-403-7208	Sequence 16896, A	Sequence 6208, AP
431	68	4.9	532	7	US-11-330-403-1984	Sequence 1984, APP	Sequence 6208, AP
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440	67.5	4.8	365	6	US-11-056-355B-68512	Sequence 68532, A	Sequence 25274, A
441	67.5	4.8	389	6	US-10-955-349-28814	Sequence 28814, A	Sequence 24222, A
442	67.5	4.8	389	7	US-11-056-355B-68511	Sequence 48531, A	Sequence 24222, A
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603	66	4.7	285	7	US-11-056-355B-10377	Sequence 102377,
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1479	6	US-11-056-355B-75679	Sequence 75679, A							
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Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.9e-117;
 Mismatches 0; Conservative 0; Indels 0; Gaps 0;

ORGANISM: Homo Sapien
 US-10-196-149-10

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Qy 121 HSGNFTGMSLYMVTILSYQMPKINGQVEMVILILIVCGVSALSMTCSSVL 180
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Qy 161 HSGNFTGLEQKLHWNPPDKGYVLHMTTAEMSMSPFGFPLTIRDFQKISLRVEAN 240
 Db 161 HSGNFTGLEQKLHWNPPDKGYVLHMTTAEMSMSPFGFPLTIRDFQKISLRVEAN 240

Qy 241 LHGLTLYDAPCPINNERTRLLSRDI 266
 Db 241 LHGLTLYDAPCPINNERTRLLSRDI 266

RESULT 3
 US-11-376-673-2
 ; Sequence 2, Application US/11376673
 ; Publication No. US20060160186A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goddard, Audrey J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND
 ; TITLE OF INVENTION: LUNG TUMOR
 ; FILE REFERENCE: P3230R1C155C
 ; CURRENT APPLICATION NUMBER: US/11/376,673
 ; CURRENT FILING DATE: 2006-03-14
 ; PRIOR APPLICATION NUMBER: 10/063742
 ; PRIOR FILING DATE: 2002-05-09
 ; PRIOR APPLICATION NUMBER: 10/006867
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/233328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: 60/170262
 ; PRIOR FILING DATE: 1999-12-09
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO: 2
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien

US-11-376-673-2
 Query Match 100.0%; Score 1392; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.9e-117; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MWFFQQGSLPLPSALVWTSAAFIIFSYTTAVTLHIDPALPYISDTGTVAPEKCLFGAML 60

Qy 61 NIAAVLCAIATIVRYKQHALSPEENVTIKLNKAIGVLGILSCLGLSVIANFQKTLFAA 120
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Qy 121 HSGAVLTGMSLYMFWTILSYQMPKIHGKQFWRLLTWGVSALSMTCSSVL 180
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 Db 181 HSGNFTGLEQKLHWNPPDKGYVLHMTTAEMSMSPFGFPLTIRDFQKISLRVEAN 240

RESULT 4
 US-11-293-697-2867
 ; Sequence 2867, Application US/11293697
 ; Publication No. US20060105376A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: HI-A0106
 ; CURRENT APPLICATION NUMBER: US/11/293,697
 ; CURRENT FILING DATE: 2005-12-05
 ; PRIOR APPLICATION NUMBER: US/10/108,266

PRIOR FILING DATE: 2002-03-28
 NUMBER OF SEQ ID NOS: 5458
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2867
 LENGTH: 238
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-293-697-2867

Query Match 34.9% Score 486.5; DB 7; Length 238;
 Best Local Similarity 38.6%; Pred. No. 3.; 8e-36;
 Matches 96; Conservative 53; Mismatches 79; Indels 21; Gaps 3;

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 Db 115 BLAVPVVDDGGALLAFVGVVVTTLQLSISYKSCPQNSLSTCHIRAVTISAVSCAAVPM 174
 Qy 174 LTCSSVLSLHSGNFGTDLQEKLNPHEDKCYKLHMITAEMSMSFSFPGFELTYIRDFOKI 233
 Db 175 IVCASLII-----TYKLENNPREKXYYVHVWSALECWTVAFGF1FYPFLTFIQDFQSV 226
 Qy 234 SURVEANLR 242
 Db 227 TLRISTEIN 235

RESULT 5
 US-11-395-249-66
 Sequence 66, Application US/11395249
 Publication No. US20060177904A1
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 APPLICANT: McCoy, John M.
 APPLICANT: Lavallie, Edward R.
 APPLICANT: Collins-Racie, Lisa A.
 APPLICANT: Evans, Cheryl
 APPLICANT: Merber, David
 APPLICANT: Treacy, Maurice
 APPLICANT: Agostino, Michael J.
 APPLICANT: Steininger II, Robert J.
 APPLICANT: Spaulding, Vicki
 APPLICANT: Wong, Gordon G.
 APPLICANT: Clark, Hilary
 APPLICANT: Pechele, Kain

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
 FILE REFERENCE: 00166.000103_6
 CURRENT APPLICATION NUMBER: US/11/395,249
 CURRENT FILING DATE: 2006-04-03
 NUMBER OF SEQ ID NOS: 240
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 66
 LENGTH: 437
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-395-249-66

Query Match 10.9% Score 151.5; DB 7; Length 437;
 Best Local Similarity 26.8%; Pred. No. 6.7e-06;
 Matches 57; Conservative 28; Mismatches 79; Indels 49; Gaps 8;

Qy 10 FLPSALVW-----TSAPIFS-----YITAVTLHHI-----DPA----- 39
 Db 46 WLSSLMTAWILLPVSLSAFSITGIVTYTAMAVMNHYTCPVENWSYNESCPPPAEQGPK 105
 Qy 40 -----LPYISDGTGTVAPEKCLFGMMLNIAAVLCIATIYVRYKQVHALSPRENVILN 92

Db 106 TCCTLDVPLISKGSPPESCOLSIGLGNMGAVALICLURGGQJBQSRRHSW---N 161
 Qy 93 KAGLVLGILSCLGLSIVANFQTKTAAHYSGAVLTFGMGSLYMFQVQTLSYQMPKIHG 152
 Db 162 TTALITGCTNAAGLIVGPNQFDHARSLYHAGAFAFPAGLFLVCLHCLSPKGPPRWT 221
 Qy 153 ----KQFVWRLLWTCV-SALSM-LTCs 177
 Db 222 WLWPICRVCMUSSPLSPWSSVESSLMRVLSCN 254

RESULT 6
 US-11-293-697-4787
 Sequence 4787, Application US/11293697
 Publication No. US2006010537A1
 GENERAL INFORMATION:
 APPLICANT: HELIX RESEARCH INSTITUTE
 TITLE OF INVENTION: Novel Full length cDNA
 FILE REFERENCE: H1-A010
 CURRENT APPLICATION NUMBER: US/11/293,697
 CURRENT FILING DATE: 2005-12-05
 PRIOR APPLICATION NUMBER: US/10/108,260
 PRIOR FILING DATE: 2004-03-28
 NUMBER OF SEQ ID NOS: 5458
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 4787

Query Match 7.1% Score 99; DB 7; Length 187;
 Best Local Similarity 23.4%; Pred. No. 0.13;
 Matches 40; Conservative 26; Mismatches 77; Indels 28; Gaps 4;

Qy 64 AVLCAITIYVRYKQVHALSPPEENVTKLNKAGLVLGILSCLGLSIVANFQTKTIAHVS 123
 Db 7 ALICL----LRYQJLQBQSRRHSW---NFTALITGCTNAAGLIVGPNQFDHARSLYH 58

Qy 124 GAVLITFGMGSLYMFQVQTLSYQMPKIHGKOVFIRULLVWCGVSALSMLTCSVYLHSG 183
 Db 59 GAGVAPPAGLFLVCHCALSTQGATAPLDIALAYLR-----SVLAVIAFITLVLSG 109

Qy 184 NGFTDLEQKLNHPEDKGYVLMHMITTAEMNSFSFRGGFLTYIRDFQKIS 234
 Db 110 VBFVHESSSQLQHG-----AALCEWTVCIDILIFYGSTVEFGAVS 149

RESULT 7
 US-11-056-355B-83608
 Sequence 83608, Application US/11056355B
 Publication No. US20060150263A1
 GENERAL INFORMATION:
 APPLICANT: Brover, Vyacheslav
 APPLICANT: Alexandrov, Nickolai
 TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 FILE REFERENCE: 2750-1590PUS2
 CURRENT APPLICATION NUMBER: US/11/056,355B
 PRIOR APPLICATION NUMBER: 60/544,190
 PRIOR FILING DATE: 2004-02-13
 NUMBER OF SEQ ID NOS: 119966
 SEQ ID NO: 83608
 LENGTH: 303
 TYPE: prt
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: (1..(303)
 OTHER INFORMATION: Ceres Seq. ID no. 12670984
 US-11-056-355B-83608

Query Match Best Local Similarity Score DB Length
 Matches 47; Conservative 21.8%; Pred. No. 0.68; 93.5; 7; 303;
 ; Mismatches 53; Indels 21; Gaps 9;

Qy 10 FLPSALVWTSAAFISYITAVLHHIDPALPYISDTGTVAPEKCLFG-AMINIAA--- 64
 Db 14 YIP--LILPSSAVSESSCSLSKYL--VLIVVLLGVITAGDNMLYSVGLIYLSASTYS 69

Qy 65 VLTATIVTRYKQVHALSPEENVITIKNAGLVGLISCLGLISIVANFQKTTLFAAHVSG 124
 Db 70 LICATQLNAVAFSYFINAQFTALLNSVLLSFSALIALNDADTPSGVSRSKYVG 129

Qy 125 AVLTFGMSLSYMFMQTYLISYQMPKIHKGKOVFIRUJLVIWCGVSALSMLTCSVTLHSGN 184
 Db 130 FVCTLAASALYSLSLMQLQFSF--KILKRETSVVLQIYTSVLA---TCVSVI--GL 182

Qy 185 FGTDLEQKLHWNPE--DKG--YVLMHMTTAAEWSM 215
 Db 183 PASGEWRTHGEMEGYTKQASYVLTWVTAIWQV 218

RESULT 8
 US-11-056-355B-83607
 ; Sequence 83607, Application US/11056355B
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; Polypeptides Encoded Thereby
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056, 355B
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544, 190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO: 83607
 ; LENGTH: 379
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE: peptide
 ; NAME/KEY: peptide
 ; LOCATION: (1); (379)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12670983
 US-11-056-355B-83607

Query Match Best Local Similarity Score DB Length
 Matches 47; Conservative 21.8%; Pred. No. 0.87; 93.5; 7; 379;
 ; Mismatches 53; Indels 21; Gaps 9;

Qy 10 FLPSALVWTSAAFISYITAVLHHIDPALPYISDTGTVAPEKCLFG-AMINIAA--- 64
 Db 90 YIP--LILPSSAVSESSCSLSKYL--VLIVVLLGVITAGDNMLYSVGLIYLSASTYS 145

Qy 65 VLTATIVTRYKQVHALSPEENVITIKNAGLVGLISCLGLISIVANFQKTTLFAAHVSG 124
 Db 146 LICATQLNAVAFSYFINAQFTALLNSVLLSFSALIALNDADTPSGVSRSKYVG 205

Qy 125 AVLTFGMSLSYMFMQTYLISYQMPKIHKGKOVFIRUJLVIWCGVSALSMLTCSVTLHSGN 184
 Db 206 FVCTLAASALYSLSLMQLQFSF--KILKRETSVVLQIYTSVLA---TCVSVI--GL 258

Qy 185 FGTDLEQKLHWNPE--DKG--YVLMHMTTAAEWSM 215
 Db 259 FASGEWRTHGEMEGYHKQASYVLTWVTAIWQV 294

RESULT 9
 US-11-056-355B-4953
 ; Sequence 4953, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:

Query Match Best Local Similarity Score DB Length
 Matches 47; Conservative 20.4%; Pred. No. 2.2; 91; Mismatches 45; Indels 102; Gaps 16;
 ; Other Information: Ceres Seq. ID no. 12364515
 ; US-11-056-355B-4953

Query Match Best Local Similarity Score DB Length
 Matches 61; Conservative 20.4%; Pred. No. 2.2; 91; Mismatches 45; Indels 102; Gaps 16;
 ; Other Information: Ceres Seq. ID no. 12364515

Query Match Best Local Similarity Score DB Length
 Matches 61; Conservative 20.4%; Pred. No. 2.2; 91; Mismatches 45; Indels 102; Gaps 16;

Qy 4 PQQGLSFLPSALVINTSAAFISYITAVLHHIDPALP--YISDGTVAPEKCLFGAML- 60
 Db 43 FPMATVYL--ALPRTTIPPAWNLA--GYVEOTIPGMVVS1GLL---LGKLLB 92

Qy 61 -----NIAAVLC----IATIYVRKQVHALSPEENVIIKLNKAGLVLG 100
 Db 93 PLWGSKELSKPFIYVNLSTSACVFNTAIVLYYTQEETIYLYTPPFSGFY-----GVYLSGL 146

Qy 101 LSCLGLSIVANFQKTTLFAAHV----SGAVLTGMSLSYMFMVOTILSYQMPKIHKGKQ 154
 Db 147 L--VGKQOLLDPQEALNLFVLIKAKWPKISLGS---FIVDFMSY-LPVULFGMY 201

Qy 155 VEWIRLLVWCGVSALSMLTCSSVLIHSGNFGTDLBOKLHNPNEDKGYVHLMITAAEWS 214
 Db 202 MSWIYRY-----FQKRRLTSLKGDPBEE----- 225

Qy 215 MSFSPFGFELTYIRDQKISRV----EANLHGTLTYDTAPCP----INNERTR 260
 Db 226 --FSFSSFFPPEFVRPLDPIASVFRLLCCRSNDARGETL-DTSPLFGSDSFANNER 281

RESULT 10
 US-11-056-355B-4952
 ; Sequence 4952, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION: Sequence Determined DNA Fragments and Corresponding
 ; Polypeptides Encoded Thereby
 ; APPLICANT: Brover, Vyacheslav
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; Polypeptides Encoded Thereby
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056, 355B
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544, 190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO: 4952
 ; LENGTH: 313
 ; TYPE: prt
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE: peptide
 ; NAME/KEY: peptide
 ; LOCATION: (1); (313)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12364514
 ; US-11-056-355B-4952

Query Match Best Local Similarity Score DB Length
 Matches 61; Conservative 20.4%; Pred. No. 2.2; 91; Mismatches 45; Indels 102; Gaps 16;

4 PQQGLSPFLPSALVITWSAAFISSYITAVTLHHIDPALP--YISDTGTVAPEKCOLFGAML- 60
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 44 FPAVTYL- ALPGRTPFPAWLITA--GYVEQTIGMVMVSIIGL--LEFGKLE 93
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 61 -----NIAAVLC----IATIIVYRYKQVTHASPEENNTIKLNKAQHVLGI 100
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 94 PLNGSKELSKRFITVNLSACVEMTAIVLYITQQETYLXTPFSGPY-----GVLSGL 147
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 101 LSCIGLISVANFQKTTLEFAAHV-----SGAVLTGCMGSIMFMVOTISYQMQPKFHGKQ 154
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 148 L--VGKQDLPQEVNLVPLKIKAKWISLVALISTLIS--FYDYMSTY-LPVLLFGMY 202.
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 155 VFWIRLILVYWCGVSAISMLTCSSVLHSGNFTDLEQKLHNWPDKGVLMNITTAAEWS 214
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 203 MSWYLYR-----FORKRLSTLKGDSE----- 226
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 215 MSFSPPFGFLTYIRDFOKISLRV-----EANLHGHTLYDTPACP-----INNERTR 260
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 227 -FSFSSPFFEFVRFPLDPIASVFHLGRSDARGETL-DTSPLQSDSFEANRRER 282
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:

RESULT 11
 US-10-449-902-35289
 ; Sequence 35289, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL LENGTH PLANT CDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 35289
 ; LENGTH: 932
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; US-10-449-902-35289

Query Match Score 6.3%; DB 6; Length 932;
 Best Local Similarity 25.2%; Pred. No. 7.5; Mismatches 38; Indels 40; Gaps 7;
 Matches 34; Conservative 23; MisMatches 38; Indels 40; Gaps 7;

Qy 90 KLINKAGLVLGILSCLGGSIVANFQKTLFAHRVSGAVLTFQKLNFTGSLYMFVQPTLSYQMQPK 149
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 500 KINASGQT---ARLGFTIA-----SATHYNG-ILEYNAHSLYGFSQIAATHQALOG 548
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 150 IHGKQVFWIRLILVYWCGVSAISMLTCSSVLHSGNFTDLEQKLHNWPDKG--YVLEM 206
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 549 LOGKRPP-----ILTRSFVGSAYAA-----HWTGDNKGTVENLRY 586
 | :|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 207 ITAAEWSMSFSFG 221
 | :|:|:|:|:|:|:|:
 Db 587 IST---MLNFGIFG 597
 | :|:|:|:|:

RESULT 13
 US-11-33-403-16766
 ; Sequence 16766, Application US/11330403
 ; Publication No. US20060159563A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S.
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement
 ; FILE REFERENCE: 38-21(53629)B
 ; CURRENT APPLICATION NUMBER: US/11/330,403
 ; CURRENT FILING DATE: 2006-01-12
 ; NUMBER OF SEQ ID NOS: 19250
 ; SEQ ID NO: 16766
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: Bacillus subtilis subsp. subtilis str. 168
 ; US-11-33-403-16766

Query Match Score 6.3%; DB 7; Length 482;
 Best Local Similarity 21.2%; Pred. No. 3.9; Mismatches 42; MisMatches 76; Indels 109; Gaps 13;
 Matches 61; Conservative 42; MisMatches 76; Indels 109; Gaps 13;

Qy 11 LPSALYTWTSAFISFSYTATVTLHHIDPALPYISDTGTV-----APEK 53
 | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 21 LRTTIVLSTPGCLLGFVDTGV---INGALDFMATAQQLNLTPTVTRGLVASSLLGAAGF 76
 | :|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 54 CLFG-----AMLNAAVLCI-----ATIVYRKOVHAL----- 81
 | :|:|:|:|:|:|:|:
 Db 77 AMFGGRGLSDRHGRRTKTLYALLFTATLGCTFESSPNASVIAFRFLGLAVGCASYTVPT 136
 | :|:|:|:|:
 Qy 82 ----SPEE--NVIIKLINKAGLVGLI-----SCGLSIVIANFORTLPAAHVSG 124
 | :|:|:|:|:
 Db 137 FLAEISPAERGRRTVONLMIVIGLHQLLFTNALTGSTGES--ANWRMLVATLPA 194
 | :|:|:|:
 Qy 125 AVLFGM-----GSALYMFVQTLISYQMQPKI-----H 151
 | :|:|:|:
 Db 195 VULWGMILVPEPSPRWLAAGRGMGDLVRQIREDSQAQEBIEKHAEGTAKAGFP 254
 | :|:|:|:

RESULT 12
 US-10-449-902-55200
 ; Sequence 55200, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.

Qy 152 GKQVFWIRLILVYWCGVSAISMLTCSSVLHSGNFTDLEQKLHNWPDKG-----HWNCP 198
 | :|:|:|:|:
 Db 255 DFQEWPWIRLIFGIGIARVOGITYGNSIMY---YCTEILREAGGFTB 299

RESULT 14
 US-10-471-571A-4918
 Sequence 4918, Application US/10471571A
 Publication No. US20060115490A1
 GENERAL INFORMATION:
 APPLICANT: CHIRON SPA
 FILE REFERENCE: P06927MO
 CURRENT APPLICATION NUMBER: US/10/471.571A
 PRIOR APPLICATION NUMBER: GB-0107661.1
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 5642
 SOFTWARE: SeqWin99, version 1.03
 SEQ ID NO: 4918
 LENGTH: 372
 TYPE: PRT
 ORGANISM: staphylococcus aureus
 FEATURE:
 NAME/KEY: MISC_FEATURE
 LOCATION: (1)..(372)
 OTHER INFORMATION: hypothetical protein
 US-10-471-571A-4918

Query Match 6.2%: Score 86; DB 6; Length 372;
 Best Local Similarity 18.1%; Prod. No. 4;
 Matches 47; Conservative 55; Mismatches 107; Indels 50; Gaps 8;

QY	1 MWFOOGLSFLPSALVI--WTSAAFIFFYITAVTLHIDPALPYISDGTVAPEKCLFGA 58
DB	26 IYFLIQGSIIOLEILMASYGIAFLPS-----LYKEKCFCIK 63
QY	59 MLNIAAVLCIATIVRYKVQVHALSPEENVIKUNKAGLVGLISCLGLISIVANFQFTLF 118
DB	64 NLDSNKLNVVSEFKIIGLILLYQNQLIL----WVAQILGLGSYMMAGVD-TAI 116
QY	119 AAHVSGAVLTFGMCSLYMFVQTILSYQMQPKTHGKOVFWRILLVINGVSALSMLTCSS 178
DB	117 KRNTNEKVQNKSNSMPLSLISIGISYLVNWKPIIMTGIF-SILTIIIRCTL 175
QY	179 VLHSGNFGTDLDEOKLHNWNPDKGYVLHMITTAEWSMSFSF----PFFFLTYIADFQKI 233
DB	176 VEN-----RELNLTGKIKKPKLPEEKWILYSPRALIIGFFGIFTI---PI 222
QY	234 SLRVEANLHGHTLYDTAPC 252
DB	223 NIYNDLKLNLNQFTSVLTC 241

RESULT 15
 US-11-128-538-37
 Sequence 37, Application US/11178538
 Publication No. US20060110792A1
 GENERAL INFORMATION:
 APPLICANT: Pausch, Mark H
 APPLICANT: Price, Laura A
 TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
 TITLE OF INVENTION: POTASSIUM: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
 CURRENT APPLICATION NUMBER: US/11178538
 CURRENT FILING DATE: 2005-07-12
 PRIOR APPLICATION NUMBER: US/08/816,011
 PRIOR FILING DATE: 1997-03-11
 PRIOR APPLICATION NUMBER: 07/332,312
 PRIOR APPLICATION NUMBER: PCT/US95/14364
 PRIOR FILING DATE: 1995-10-25
 NUMBER OF SEQ ID NOS: 67
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 37
 LENGTH: 481

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OM protein - protein search, using SW model

Run on: August 28, 2006, 17:37:50 ; Search time 184 Seconds

(without alignments)

669.648 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

Sequence: 1 MWTFQGLSFLPSALIVITS.....YDTAPCPINNERTLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA Main:*

1: /BMC_Celerra_SIDB3/picodata/2/pubcaa/US07_PUBCOMB_pep:*
 2: /BMC_Celerra_SIDB3/picodata/2/pubcaa/US08_PUBCOMB_pep:*
 3: /BMC_Celerra_SIDB3/picodata/2/pubcaa/US09_PUBCOMB_pep:*
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 5: /BMC_Celerra_SIDB3/picodata/2/pubcaa/US10B_PUBCOMB_pep:*
 6: /BMC_Celerra_SIDB3/picodata/2/pubcaa/US11_PUBCOMB_pep:*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1392	100.0	266	3 US-09-989-722-23	Sequence 23, App1
2	1392	100.0	266	3 US-09-988-723-23	Sequence 23, App1
3	1392	100.0	266	3 US-09-988-729-23	Sequence 23, App1
4	1392	100.0	266	3 US-09-988-727-23	Sequence 23, App1
5	1392	100.0	266	3 US-09-988-731-23	Sequence 23, App1
6	1392	100.0	266	3 US-09-988-732-23	Sequence 23, App1
7	1392	100.0	266	3 US-09-991-073-23	Sequence 23, App1
8	1392	100.0	266	3 US-09-994-442-23	Sequence 23, App1
9	1392	100.0	266	3 US-09-991-163-23	Sequence 23, App1
10	1392	100.0	266	3 US-09-993-604-23	Sequence 23, App1
11	1392	100.0	266	3 US-09-994-456-23	Sequence 23, App1
12	1392	100.0	266	3 US-09-988-721-23	Sequence 23, App1
13	1392	100.0	266	3 US-09-992-598-23	Sequence 23, App1
14	1392	100.0	266	3 US-09-988-293A-23	Sequence 23, App1
15	1392	100.0	266	3 US-09-988-735-23	Sequence 23, App1
16	1392	100.0	266	3 US-09-990-444-23	Sequence 23, App1
17	1392	100.0	266	3 US-09-991-181-23	Sequence 23, App1
18	1392	100.0	266	3 US-09-988-730-23	Sequence 23, App1
19	1392	100.0	266	3 US-09-990-436-23	Sequence 23, App1
20	1392	100.0	266	3 US-09-993-687-23	Sequence 23, App1
21	1392	100.0	266	3 US-09-988-734-23	Sequence 23, App1
22	1392	100.0	266	3 US-09-990-653-23	Sequence 23, App1
23	1392	100.0	266	3 US-09-988-724-23	Sequence 23, App1
24	1392	100.0	266	3 US-09-988-728-23	Sequence 23, App1
25	1392	100.0	266	3 US-09-990-441-23	Sequence 23, App1
26	1392	100.0	266	3 US-09-993-667-23	Sequence 23, App1
27	1392	100.0	266	3 US-09-997-428-23	Sequence 23, App1
28	1392	100.0	266	3 US-09-997-6666-23	Sequence 23, App1
29	1392	100.0	266	3 US-09-990-436-23	Sequence 23, App1
30	1392	100.0	266	3 US-09-990-562-23	Sequence 23, App1
31	1392	100.0	266	3 US-09-974-879-147	Sequence 147, App1
32	1392	100.0	266	3 US-09-990-711-23	Sequence 23, App1
33	1392	100.0	266	3 US-09-989-776-23	Sequence 23, App1
34	1392	100.0	266	3 US-09-998-156-23	Sequence 23, App1
35	1392	100.0	266	3 US-09-991-157-23	Sequence 23, App1
36	1392	100.0	266	3 US-09-991-151-23	Sequence 23, App1
37	1392	100.0	266	3 US-09-997-514-23	Sequence 23, App1
38	1392	100.0	266	3 US-09-997-513-23	Sequence 23, App1
39	1392	100.0	266	3 US-09-991-172-23	Sequence 23, App1
40	1392	100.0	266	3 US-09-990-776-23	Sequence 23, App1
41	1392	100.0	266	3 US-09-997-683-23	Sequence 23, App1
42	1392	100.0	266	3 US-09-989-559-23	Sequence 23, App1
43	1392	100.0	266	3 US-09-997-601-23	Sequence 23, App1
44	1392	100.0	266	3 US-09-990-440-23	Sequence 23, App1
45	1392	100.0	266	3 US-09-997-857-23	Sequence 23, App1
46	1392	100.0	266	3 US-09-993-467-23	Sequence 23, App1
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689	1392	100.0	266	4	US-10-063-660-2	Sequence 2, Appli	762	1388	99.7	267	3	US-09-978-360A-702
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ALIGNMENTS

RESULT 1
 US-09-989-722-23
 US-00020072067A1
 / GENERAL INFORMATION:
 / Patent No. US20020072067A1
 / APPICANT: Ashkenazi, Avi J.
 / APPICANT: Baker, Kevin P.
 / APPICANT: Botstein, David
 / APPICANT: Desnoyers, Luc
 / APPICANT: Eason, Dan L.
 / APPICANT: Ferrara, Napoleone
 / APPICANT: Fong, Sherman
 / APPICANT: Gerber, Hanspeter
 / APPICANT: Gerriksen, Mary E.
 / APPICANT: Goddard, Audrey
 / APPICANT: Grimaldi, Paul J.
 / APPICANT: Grimaldi, J. Christopher
 / APPICANT: Gurney, Austin L.
 / APPICANT: Klijaviv, Ivor J.
 / APPICANT: Napier, Mary A.
 / APPICANT: Pan, James
 / APPICANT: Paoni, Nicholas F.
 / APPICANT: Roy, Margaret Ann
 / APPICANT: Stewart, Timothy A.
 / APPICANT: Tumas, Daniel
 / APPICANT: Watanahe, Colin K.
 / APPICANT: Williams, P. Mickey
 / APPICANT: Wood, William I.
 / APPICANT: Zemlin, Zhang
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 / FILE REFERENCE: P2730PIC63
 / CURRENT APPLICATION NUMBER: US/09/989,722
 / CURRENT FILING DATE: 2001-11-19
 / PRIOR APPLICATION NUMBER: 60/049787
 / PRIOR FILING DATE: 1997-06-16
 / PRIOR APPLICATION NUMBER: 60/062250
 / PRIOR FILING DATE: 1997-10-17
 / PRIOR APPLICATION NUMBER: 60/075945
 / PRIOR FILING DATE: 1998-02-15
 / PRIOR APPLICATION NUMBER: 60/065311
 / PRIOR FILING DATE: 1998-03-20
 / PRIOR APPLICATION NUMBER: 60/066770
 / PRIOR FILING DATE: 1998-04-28
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 / PRIOR FILING DATE: 1998-06-01

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PRIOR APPLICATION NUMBER: 60/091975
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-02

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; PRIOR FILING DATE: 1998-07-09
Query Match 100.0%: Score 1.392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-12;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      241 LHGLTYDTPCPINNERTRLSRDI 266

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RESULT 2

US 09-989-723-23

Sequence 23, Application US/09898723

Patent No. US20020072092A1

GENERAL INFORMATION

Applicant: Ashkenazi, Avi J.

Applicant: Baker, Kevin P.

Applicant: Botstein, David

Applicant: Desnoyers, Luc

Applicant: Eaton, Dan L.

Applicant: Ferrara, Napoleone

Applicant: Fong, Sherman

Applicant: Gerber, Hanspeter

Applicant: Gerritsen, Mary E.

Applicant: Goddard, Audrey

Applicant: Godowski, Paul J.

Applicant: Grimaldi, J Christopher

Applicant: Gurney, Austin L.

Applicant: Kljavin, Ivar J.

Applicant: Napier, Mary A.

Applicant: Pan, James

Applicant: Paoni, Nicholas F.

Applicant: Roy, Margaret Ann

Applicant: Stewart, Timothy A.

Applicant: Tumas, Daniel

Applicant: Watanabe, Colin K.

Applicant: Williams, P. Mickey

Applicant: Wood, William I.

Applicant: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730PIC62

CURRENT APPLICATION NUMBER: US/09/989,723

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

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 PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5.1e-127;
 Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MWFFQGLSFLPSALVWTSAAFISYITAVLHIDPALYISTGTGVAPEKCLFGAML 60
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Qy	61 NIAAVLICIAIIVRYRKQVHALSPENENVILINKAGAVLGUSLGSIVANFQQTTLFAA 120
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Db	181 HSGNFGTDLBEQLHNPEDKGYVLMNITTAEWSMSFSFPEFLTYIRDFOKISRVEAN 240
Qy	241 LHGLTLYDTAFCPINNERTLLSDI 266
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RESULT 3
 US-09-989-279-23
 Sequence 23, Application US/09989279
 Patent No. US20020072496A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerriksen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Klayvin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ACIDS Encoding the Same
 FILE REFERENCE: P2730PIC56
 CURRENT APPLICATION NUMBER: US/09/989,279
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-06-16

PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091636
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5.1e-12;
 Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MWFFQQISFLPSALVWTSAAPIFSTYTAATLHHIDPALPVISDTGTAVPEKCLFGAML 60
Db	1 MWFFQQISFLPSALVWTSAAPIFSTYTAATLHHIDPALPVISDTGTAVPEKCLFGAML 60
Qy	61 NIAAVLCAITIYRYKQWHALSPEENTIKLNKAGLVIGLIGLISCLGLSIVANFQTKTLEA 120
Db	61 NIAAVLCAITIYRYKQWHALSPEENTIKLNKAGLVIGLIGLISCLGLSIVANFQTKTLEA 120
Qy	121 HVSQAVTJFGMSLYMFQYQTLISYQMPKHKQVFWTRIJIUVIWCSSYVALSMLTCSSVL 180
Db	121 HVSQAVTJFGMSLYMFQYQTLISYQMPKHKQVFWTRIJIUVIWCSSYVALSMLTCSSVL 180
Qy	181 HSGNFGTLEQKLNHNPDKGYLHMTTAEMSMSFFGGFLTYIRDFQKISLRVEAN 240
Db	181 HSGNFGTLEQKLNHNPDKGYLHMTTAEMSMSFFGGFLTYIRDFQKISLRVEAN 240
Qy	241 LHGLTLYDTPCPINNETRLRSRD 266
Db	241 LHGLTLYDTPCPINNETRLRSRD 266

RESULT 4

US-09-989-727-23
 Sequence 23, Application US/09989727
 Patent No. US2002002497A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Deanoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goodard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J.Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kliaviv, Ivar J.
 APPLICANT: Napior, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tunas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
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 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
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 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25

Query Match 100.0%; Score 1392; DB 3; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5.1e-127;
 Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWFFQQLSFPSALWTTSAFISIXTATVTLHHDPALPYISDGTVAEBCKLGAML 60
 Db 1 MWFFQQLSFPSALWTTSAFISIXTATVTLHHDPALPYISDGTVAEBCKLGAML 60

Qy 61 NIAAVLICATIIVYRKQVHALSPENVITKLNAKLGVIGLISCLGLSIVANFQKTTLFAA 120
 Db 61 NIAAVLICATIIVYRKQVHALSPENVITKLNAKLGVIGLISCLGLSIVANFQKTTLFAA 120

Qy 1.21 HVSGAVLTFGMSLIMFVQTILSYQONPKIHKGKFQWIRLILVWCGVSLMSLTCSVL 180
 Db 1.21 HVSGAVLTFGMSLIMFVQTILSYQONPKIHKGKFQWIRLILVWCGVSLMSLTCSVL 180

Qy 181 HSGNFTGTDLEQLNHNPEDKGYVLLMITTAEWSFSFRGFLTYIRDFOXISLRVEAN 240
 Db 181 HSGNFTGTDLEQLNHNPEDKGYVLLMITTAEWSFSFRGFLTYIRDFOXISLRVEAN 240

Qy 241 LHGLTYDTAPCPINNERTRLSRDI 266
 Db 241 LHGLTYDTAPCPINNERTRLSRDI 266

RESULT 5
 US-09-989-731-23
 Sequence 23, Application US/09989731
 ; Patent No. US0020103125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hans Peter
 ; APPLICANT: Geritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurin, Austin L.
 ; APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumms, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730P1C70

CURRENT APPLICATION NUMBER: US/09/989,731

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

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PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087827

PRIOR FILING DATE: 1998-06-03

PRIOR APPLICATION NUMBER: 60/088021

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088025

PRIOR FILING DATE: 1998-06-04

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 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0% Score 1392; DB 3; Length 266;

Best Local Similarity 100.0% Pred. No. 5.le-17;
 Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWFFQQGISFLPSALVINTSAAFISYTAVTLHIDPALPYISDTGTVAPEKCLFGAML 60
 Db 1 MWFFQQGISFLPSALVINTSAAFISYTAVTLHIDPALPYISDTGTVAPEKCLFGAML 60
 Db 1 HVSAGAVLFGMGLYMFQTILSYQMQPKIHGQVFWRLLVWCGTALSMLTCSSVL 180
 Db 1 HVSAGAVLFGMGLYMFQTILSYQMQPKIHGQVFWRLLVWCGTALSMLTCSSVL 180
 Qy 61 NIARVLCATIYYRYKQVHALSPRENNVIKLANKAGLVIGLIGS1STVANFOKTTLFAA 120
 Db 61 NIARVLCATIYYRYKQVHALSPRENNVIKLANKAGLVIGLIGS1STVANFOKTTLFAA 120
 Qy 121 HSGNFTGTDLEQKLNPNPDKGYLHMTTAEWSMSFSSFFGPFPLTYIRDFOKISLRVEAN 240
 Db 121 HSGNFTGTDLEQKLNPNPDKGYLHMTTAEWSMSFSPFGFETYIRDFOKISLRVEAN 240
 Qy 241 LHGLTLYDTPACPINNERTLRSIDI 266
 Db 241 LHGLTLYDTPACPINNERTLRSIDI 266

RESULT 6

US-09-369-732-23
 Sequence 23, Application US/09989732
 General Information:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoléone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hans Peter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Klijavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas P.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC57
 CURRENT APPLICATION NUMBER: US/09/989,732
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-15
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MWFWFOQSLPSLAVLWTSAAFISSVITAVLHHIDPALPYISDTGTVAPKCLFGAML 60
1 MWFWFOQSLPSLAVLWTSAAFISSVITAVLHHIDPALPYISDTGTVAEKCLFGAML 60
61 NIAAVICLTIYRKQVHALSPEENVIKLINKAGLVGLSIVANFQKTLFAA 120
61 NIAAVICLTIYRKQVHALSPEENVIKLINKAGLVGLSIVANFQKTLFAA 120
Db 121 HVSGAVLTFGMSLIMFVQTLISYQMQPKINGKQFWIRLLIVCGVSALSMTCSSVL 180
Db 121 HVSGAVLTFGMSLIMFVQTLISYQMQPKINGKQFWIRLLIVCGVSALSMTCSSVL 180
Qy 181 HSGNFGTDLTEQKLHNFBDKGTVLNTTANEWSMSTSFFGFPLTYIRDQKISRVEAN 240
Db 181 HSGNFGTDLTEQKLHNFBDKGTVLNTTANEWSMSTSFFGFPLTYIRDQKISRVEAN 240
Qy 241 LHGLTLYDTAPCPINNERTRLLSRDI 266
Db 241 LHGLTLYDTAPCPINNERTRLLSRDI 266

RESULT 7

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US-09-991-073-23 Sequence 23, Application US/0991073
Patent No. US20020127576A1.
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Dennoyer, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Perrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Godowski, Audrey
APPLICANT: Gooldski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kjavian, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pao, James
APPLICANT: Pacini, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Trapped
Title of Invention: Acids Encoding
FILE REFERENCE: P2730P1C15
CURRENT APPLICATION NUMBER: US/09/9
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred No. 5.1e-127; Indels 0; Gaps 0;
Matches 266; Conservative 0;

Db 181 HSGNFTDLEQKLHWNPDKGYVLMITTAENSMSFSSFGFLTYIRDQKISLVEAN 240
Qy 241 LHGLTYDAPCPINNERTRLLSRI 266
Db 241 LHGLTYDAPCPINNERTRLLSRI 266

RESULT 8
US-09-990-442-23
; Sequence 23, Application US/09990442
; Patent No. US2002013252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klijavink, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
FILE REFERENCE: P2730P1C8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Db 61 NIAAVLCAIATIVRYKQVHALSPENVTKLNKAGLVGILSCLGSLVANFOKTTLFAA 120

Qy 121 HVSGAVLTFGMGSLYMFVDTLSIQMPPKIHGKOVFWRLLVWCGTSALSMLTCSV 180
Db 121 HVSGAVLTFGMGSLYMFVDTLSIQMPPKIHGKOVFWRLLVWCGTSALSMLTCSV 180

Qy 181 HSGNFTDLEQKLHWNPDKGYVLMITTAENSMSFSSFGFLTYIRDQKISLVEAN 240

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Qy 181 HSGNFGTLEQKLHWNEDPKGYVLMITTAEWMSMSESFFGFLTYRDFOKISRVEAN 240
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 i GENERAL INFORMATION
 i APPLICANT: Ashkenazi, Avi J.
 i APPLICANT: Baker, Kevin P.
 i APPLICANT: Borstein, David
 i APPLICANT: Desnoyers, Luc
 i APPLICANT: Eaton, Dan L.
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 i APPLICANT: Tumas, Daniel
 i APPLICANT: Watanabe, Colin K.
 i APPLICANT: Williams, P. Mickey
 i APPLICANT: Wood, William I.
 i APPLICANT: Zhang, Zemin
 i TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 i FILE REFERENCE: P230P1C17
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PRIOR APPLICATION NUMBER: 60/092182

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Query Match      100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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    1 MWVFCQGLSPLSALVITWSAAFISSYITAVTLHHIDPALPVISDTGVAPEKCLFGAML 60
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Qy   61 NIAAVLCLIAATTIVRYKQVHALSPEENVIIKLINKAGLVGLGILSCLGLISIVANFORTLFAA 120
Db   121 HVSGAVLTGFMGSLSIMFVQTLISYQMPKTHGKQFWIRLLIVWCCVSALSMLTCSSVL 180
    121 HVSGAVLTGFMGSLSIMFVQTLISYQMPKTHGKQFWIRLLIVWCCVSALSMLTCSSVL 180
Qy   121 HVSGAVLTGFMGSLSIMFVQTLISYQMPKTHGKQFWIRLLIVWCCVSALSMLTCSSVL 180
Db   181 HSGNFGTDLBQKLHNPKDGYVLMIMTTAEWSMSFSFFGPFLTYRDQKTSRVEAN 240
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Qy   181 HSGNFGTDLBQKLHNPKDGYVLMIMTTAEWSMSFSFFGPFLTYRDQKTSRVEAN 240
Db   241 LHGLTLTLYDAPCPINNERTLLSRDI 266
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RESULT 10

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US-09-993-604-23
; Sequence 23, Application US/09993604
; PATENT No. US20020137075A1
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi, Avi J.
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan L.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gerber, Hanspeter
;   APPLICANT: Gerritsen, Mary E.
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Goodowski, Paul J.
;   APPLICANT: Grimaldi, J. Christopher
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Kijaviv, Ivar J.
;   APPLICANT: Napior, Mary A.
;   APPLICANT: Pan, James
;   APPLICANT: Paoni, Nicholas F.
;   APPLICANT: Roy, Margaret Ann
;   APPLICANT: Stewart, Timothy A.
;   APPLICANT: Tumans, Daniel
;   APPLICANT: Watanabe, Colin K.
;   APPLICANT: Williams, P. Mickey
;   APPLICANT: Wood, William I.
;   APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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Query Match 100.0%; Score 1392; DB 3; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5.1e-12;
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Qy	Db	121 HVGAVLTLFGMGSLYMFQTILSYQMQPKHGVFMRLLYIWCGYSAISMLTCSSVL 180	121 HVGAVLTLFGMGSLYMFQTILSYQMQPKHGVFMRLLYIWCGYSAISMLTCSSVL 180
Qy	Db	121 HVGAVLTLFGMGSLYMFQTILSYQMQPKHGVFMRLLYIWCGYSAISMLTCSSVL 180	181 HSGNFGTLEQKUHWNPDKGTVLHMTTAEWSMSFSEFFFLTYIRDFOQKISLRVEAN 240
Qy	Db	181 HSGNFGTLEQKUHWNPDKGTVLHMTTAEWSMSFSEFFFLTYIRDFOQKISLRVEAN 240	241 LHGHTLYDTAPCPINNEETRLRSRD1 266
Qy	Db	241 LHGHTLYDTAPCPINNEETRLRSRD1 266	241 LHGHTLYDTAPCPINNEETRLRSRD1 266

RESULT 11
 US-09-990-456-23
 ; Sequence 23, Application US/0990456
 ; Patent No. US2002017890A1

GENERAL INFORMATION:

- APPLICANT: Ashkenazi, Avi J.
- APPLICANT: Baker, Kevin P.
- APPLICANT: Botstein, David
- APPLICANT: Desnoyers, Luc
- APPLICANT: Eaton, Dan L.
- APPLICANT: Ferrara, Napoleone
- APPLICANT: Fong, Sherman
- APPLICANT: Gerber, Hanspeter
- APPLICANT: Gerritsen, Mary E.
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul J.
- APPLICANT: Grimaldi, J. Christopher
- APPLICANT: Gurney, Austin L.
- APPLICANT: Kijavin, Ivar J.
- APPLICANT: Napier, Mary A.
- APPLICANT: Pan, James
- APPLICANT: Paoni, Nicholas F.
- APPLICANT: Roy, Margaret Ann
- APPLICANT: Stewart, Timothy A.
- APPLICANT: Tumas, Daniel
- APPLICANT: Watanahe, Colin K.
- APPLICANT: Williams, P. Mickey
- APPLICANT: Wood, William I.
- APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P230P1C22

CURRENT APPLICATION NUMBER: US/09/990,456

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1998-06-26

; Query Match Score 1392; DB 3; Length 266;
; Best Local Similarity 100.0%; Pred. No. 5.1e-127;
; Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 HVSGAVLTFGMSLNMVQTLLSKYQMPKTHGKQFWIRLILVVGVSALSMLTCSSVL 180
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Qy 181 HSGNFGTDLDEQLHWNPDKGYVLMIMTTAEWSMSFFFLTYIRDFOKISRVEAN 240
Db 181 HSGNFGTDLDEQLHWNPDKGYVLMIMTTAEWSMSFFFLTYIRDFOKISRVEAN 240
Qy 241 LHGLTLYDТАPCPINNERTLLSDRI 266
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; Sequence 23, Application US/09989721
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klijavin, Iver J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nichols F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanae, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
;
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P230P1C55

CURRENT APPLICATION NUMBER: US/09/989,721

CURRENT FILING DATE: 2001-11-19

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 PRIOR FILING DATE: 1998-07-09

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Db	121	HVGSAVLFGMGSLYMFQTILSYQMKPIHKQVFWTRLLVIVCGVSALSMLTCSSVL 180
Qy	181	HSGNFGTDLBOKLHNPEDKGYVLMITTAENSMSFSFFGGFLTYIRDFOKISLRVEAN 240
Db	181	HSGNFGTDLBOKLHNPEDKGYVLMITTAENSMSFSFFGGFLTYIRDFOKISLRVEAN 240
Qy	241	LHGHTLYDTPAPCPINNESTRRLSRDI 266
Db	241	LHGHTLYDTPAPCPINNESTRRLSRDI 266

RESULT 13
 US-09-992-598-23
 Sequence 23, Application US/0992598
 Patent No. US2002016384A1

GENERAL INFORMATION:

- APPLICANT: Ashkenazi, Avi J.
- APPLICANT: Baker, Kevin P.
- APPLICANT: Borstein, David
- APPLICANT: Desnoyers, Luc
- APPLICANT: Bacon, Dan L.
- APPLICANT: Ferrara, Napoleone
- APPLICANT: Fong, Sherman
- APPLICANT: Gerber, Hanspeter
- APPLICANT: Gerritsen, Mary E.
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul J.
- APPLICANT: Grimaldi, J. Christopher
- APPLICANT: Gurney, Austin L.
- APPLICANT: Kijavin, Ivar J.
- APPLICANT: Napier, Mary A.

PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-07-19

Query Match 100.0%; Score 1392; DB 3; Length 266;
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Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 HSGNFGTDLQKLHNPBDKGYUMLIMITTAELMSMSPSFPPFLITYRDFOKISLRVEAN 240
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Qy 241 LHGLTLYDTAPCPINNERTLISLDI 266
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RESULT 14
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; Patent No. US200201716A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

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APPLICANT: Fong, Sherman          / PRIOR APPLICATION NUMBER: 60/088217
APPLICANT: Gerber, Hanspeter      / PRIOR FILING DATE: 1998-06-05
APPLICANT: Gerritsen, Mary E.      / PRIOR APPLICATION NUMBER: 60/088655
APPLICANT: Goddard, Audrey        / PRIOR FILING DATE: 1998-06-09
APPLICANT: Godowski, Paul J.       / PRIOR APPLICATION NUMBER: 60/088734
APPLICANT: Grimaldi, J. Christopher / PRIOR FILING DATE: 1998-06-10
APPLICANT: Gurney, Austin L.       / PRIOR APPLICATION NUMBER: 60/088738
APPLICANT: Kljavin, Ivar J.        / PRIOR FILING DATE: 1998-06-10
APPLICANT: Napier, Mary A.         / PRIOR APPLICATION NUMBER: 60/088742
APPLICANT: Pan, James             / PRIOR FILING DATE: 1998-06-10
APPLICANT: Paoni, Nicholas F.      / PRIOR APPLICATION NUMBER: 60/088810
APPLICANT: Roy, Margaret Ann      / PRIOR FILING DATE: 1998-06-10
APPLICANT: Stewart, Timothy A.     / PRIOR APPLICATION NUMBER: 60/088824
APPLICANT: Tumas, Daniel           / PRIOR FILING DATE: 1998-06-10
APPLICANT: Watanabe, Colin K.       / PRIOR APPLICATION NUMBER: 60/088826
APPLICANT: Williams, P. Mickey     / PRIOR FILING DATE: 1998-06-10
APPLICANT: Wood, William I.         / PRIOR APPLICATION NUMBER: 60/088858
APPLICANT: Zhang, Zemin            / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                  / FILE REFERENCE: P230PIC66
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Db      1 MWFWQQSLPSALVWTSAAFISYITAVLHHIDPALPYISDTGTVAPBKCLFGAML 60
Qy      61 NIAAVLCIATIYVRKVHALSPENVITKLNKGVLGILSCLGSIIVANFQKTTLFAA 120
Db      61 NIAAVLCIATIYVRKVHALSPENVITKLNKGVLGILSCLGSIIVANFQKTTLFAA 120
Qy      121 HYSGAVLTFGMGLSYMFMVQTLISYQMPKINGKQFWIRLLIVWCCVSALSMTCSSVL 180
Db      121 HYSGAVLTFGMGLSYMFMVQTLISYQMPKINGKQFWIRLLIVWCCVSALSMTCSSVL 180
Qy      181 HSGNFGTDLQEKLHWNPEDKGYLHMITTAEWSMSFSFFGGFLTYIRDFOKISRVEAN 240

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Mon Sep 11 16:53:58 2006

us-10-006-867-2.spdi.rapbm

Page 35

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Qy 241 LHGLTLYDTAPCPINNERTRLLSRDI 266
Db 241 LHGLTLYDTAPCPINNERTRLLSRDI 266

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Job time : 209 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using SW model

Run on: August 28, 2006, 17:32:09 ; Search time 41 Seconds

(without alignments)

624.236 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9616763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR 80:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	288	20.7	2 T1654	hypothetical prote
3	120	8.6	547 C88456	protein W0A5.2 [i
4	103	7.4	332 B69312	nitrate reductase
5	98.5	7.1	1120 A10561	integral membrane
6	97	7.0	604 B75253	carbon starvation
7	96	6.9	495 S43882	NADH2 dehydrogenas
8	94	6.8	495 S16447	hypothetical prote
9	93.5	6.7	379 D96506	probable protein
10	93.5	6.7	429 F71651	putrescine-ornithi
11	93	6.7	1120 E86194	mechanosensitive C
12	93	6.7	1120 B85544	mechanosensitive C
13	93	6.7	1120 H64776	probable membrane
14	92.5	6.6	492 A0801	probable amino aci
15	91.5	6.6	373 T24487	hypothetical prote
16	91.5	6.6	712 T02479	potassium transpor
17	90.5	6.5	614 G71019	hypothetical prote
18	90	6.5	400 C82503	hypothetical prote
19	90	6.5	492 S59107	NADH2 dehydrogenas
20	90	6.5	528 S19366	hypothetical prote
21	89.5	6.4	440 B64090	dicarboxylate tran
22	89.5	6.4	443 AB1706	hypothetical prote
23	89	6.4	495 E86194	hypothetical prote
24	89.5	6.4	599 T24333	hypothetical prote
25	89	6.4	428 A10334	probable transmembr
26	89	6.4	757 T42293	hypothetical prote
27	88.5	6.4	430 E75217	transporter PAB21.7
28	88.5	6.4	844 T23556	hypothetical prote
29	88	6.3	1165 A46180	adenylyl cyclase t

30	87.5	6.3	233 E70114	hemolysin III (ypl
31	87.5	6.3	429 G2	GGDEF family prote
32	87	6.3	482 B69803	metabolite transpo
33	87.5	6.3	540 T24675	hypothetical prote
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35	87	6.2	396 D85857	bicyclomycin resin
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37	87	6.2	613 C83496	glucathione-regula
38	86.5	6.2	400 C69757	transporter homolo
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68	83	6.0	460 D75106	hypothetical prote
69	83	6.0	496 B83503	probable amino aci
70	83	6.0	637 S01509	NADH2 dehydrogenas
71	82.5	5.9	391 S48967	ethanolamine/nephosph
72	82.5	5.9	452 A71877	probable aromatic tr
73	82.5	5.9	494 T14246	proline/betaine tr
74	82.5	5.9	596 75	cytochrome-c oxida
75	82.5	5.9	596 76	probable amino aci
76	82	5.9	317 77	hypothetical prote
77	82	5.9	327 78	probable ABC trans
78	82	5.9	356 79	purine permease [i
79	82	5.9	446 80	citrate transport
80	82	5.9	461 81	probable potassium
81	82	5.9	461 82	conserved hypotet
82	82	5.9	548 83	cytochrome-c oxida
83	82	5.9	548 84	sugar ABC transpor
84	82	5.9	548 85	hypothetical prote
85	82	5.9	548 86	hypothetical prote
86	81.5	5.9	205 87	hypothetical prote
87	81.5	5.9	205 88	hypothetical prote
88	81.5	5.9	292 89	NADH2 dehydrogenas
89	81.5	5.9	307 90	hypothetical prote
90	81.5	5.9	307 91	hypothetical prote
91	81.5	5.9	307 92	T41583
92	81.5	5.9	307 93	T23589
93	81.5	5.9	307 94	C86408
94	81.5	5.9	307 95	B83017
95	81	5.9	307 96	D71517
96	81	5.9	307 97	H85822
97	81	5.9	307 98	T24677
98	81	5.9	307 99	C64878
99	81	5.9	307 100	hypothetical prote
100	81	5.9	307 101	hypothetical prote
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102	81	5.9	307 103	hypothetical prote
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108	81	5.9	307 109	hypothetical prote
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119	81	5.9	307 120	hypothetical prote
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128	81	5.9	307 129	hypothetical prote
129	81	5.9	307 130	hypothetical prote
130	81	5.9	307 131	hypothetical prote
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135	81	5.9	307 136	hypothetical prote
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196	81	5.9	307 197	hypothetical prote
197	81	5.9	307 198	hypothetical prote

103	80.5	359	2	F90055	5.6	176	77.5	A72771
104	80.5	385	2	T07130	5.6	177	77.5	461
105	5.8	433	2	AC043	5.6	178	77.5	C83605
106	80.5	5.8	473	G69789	5.6	179	77.5	464
107	80.5	5.8	528	E81186	5.6	180	77.5	479
108	80.5	5.8	590	QBYPR	5.6	181	77.5	A90863
109	80.5	637	2	S79171	5.6	182	77.5	AG0882
110	80.5	5.8	728	T13794	5.6	183	77.5	F64862
111	80	5.7	266	GB178	5.6	184	77.5	D96744
112	80	5.7	291	A97387	5.6	185	77.5	E71695
113	80	5.7	291	AB2605	5.6	186	77.5	A82432
120	79.5	5.7	445	S77010	5.6	187	77.5	T01853
114	80	5.7	429	C41903	5.6	188	77.5	D95973
115	80	5.7	702	T12141	5.6	189	77.5	S49345
116	80	5.7	902	C83064	5.6	190	77.5	S76103
117	80	5.7	1123	T48586	5.6	191	77.5	A69478
118	79.5	5.7	323	T32279	5.6	192	77.5	B. subtilis YxkD p
119	79.5	5.7	405	T42292	5.6	193	77.5	probable sugar uptake
121	79.5	5.7	445	F75059	5.6	194	77.5	cytochrome-c oxidase
122	79.5	5.7	499	1	5.6	195	77.5	hypothetical protein
123	79.5	5.7	539	S49195	5.6	196	77.5	NADH2 dehydrogenases
124	79.5	5.7	542	AG3605	5.6	197	77.5	phenylalanine amino acid permease
125	79.5	5.7	570	AH2765	5.6	198	77.5	shikimate transporter
126	79.5	5.7	598	E97546	5.6	199	77.5	amino acid permease
127	79.5	5.7	741	T13051	5.6	200	77.5	amino acid permease
128	79	5.7	831	B40204	5.6	201	77.5	phosphate transport
129	79	5.7	172	F75015	5.6	202	77.5	membrane protein
130	79	5.7	173	AG4009	5.6	203	77.5	hypothetical integral membrane protein
131	79	5.7	281	T26244	5.6	204	77.5	cytochrome-c oxidase
132	79	5.7	293	B83783	5.6	205	77.5	hypothetical protein
133	79	5.7	293	H72064	5.6	206	76.5	ABC transporter, P
134	79	5.7	293	C86558	5.6	207	76.5	metal transport protein
135	79	5.7	307	CB1862	5.6	212	76.5	NADH2 dehydrogenase
136	79	5.7	377	T49063	5.6	213	76.5	hypothetical protein
137	79	5.7	390	H72265	5.6	208	76.5	hypothetical protein
138	79	5.7	395	T31717	5.6	209	76.5	hypothetical protein
144	79	5.7	410	D69112	5.6	210	76.5	hypothetical protein
145	79	5.7	438	E84998	5.6	211	76.5	hypothetical protein
146	79	5.7	444	B90976	5.6	212	76.5	hypothetical protein
147	79	5.7	453	GB2392	5.6	213	76.5	hypothetical protein
148	79	5.7	473	T31717	5.6	214	76.5	hypothetical protein
149	79	5.7	489	B9789	5.6	215	76.5	hypothetical protein
150	78.5	5.6	405	T12339	5.6	216	76.5	hypothetical protein
156	78.5	5.6	685	G69801	5.6	217	76.5	hypothetical protein
151	78.5	5.6	819	T20371	5.6	218	76.5	hypothetical protein
152	78.5	5.6	913	F75113	5.6	219	76.5	hypothetical protein
153	78.5	5.6	169	H84491	5.6	220	76.5	hypothetical protein
154	78.5	5.6	241	S00836	5.6	221	76.5	hypothetical protein
155	78.5	5.6	366	C64449	5.6	222	76.5	hypothetical protein
156	78.5	5.6	405	T266718	5.6	223	76.5	hypothetical protein
157	78.5	5.6	412	G89773	5.6	224	76.5	hypothetical protein
158	78.5	5.6	493	F70513	5.6	225	76.5	NADH2 dehydrogenase
159	78	5.6	579	A70954	5.6	226	76.5	hypothetical protein
160	78	5.6	622	E69009	5.6	227	76.5	hypothetical protein
161	78	5.6	624	T48587	5.6	228	76.5	hypothetical protein
162	78	5.6	732	T13814	5.6	229	76.5	NADH2 dehydrogenase
163	78	5.6	744	T13485	5.6	230	76.5	hypothetical protein
164	78	5.6	1325	A0795	5.6	231	76.5	hypothetical protein
165	78	5.6	158	T26519	5.6	232	76	hypothetical protein
166	78	5.6	307	D81082	5.6	233	76	hypothetical protein
167	78	5.6	422	T48661	5.6	234	76	hypothetical protein
168	78	5.6	335	E81736	5.6	235	76	hypothetical protein
169	78	5.6	688	T06299	5.6	236	76	hypothetical protein
170	77.5	5.6	701	T15238	5.6	237	76	hypothetical protein
171	77.5	5.6	283	E83916	5.6	238	76	hypothetical protein
172	77.5	5.6	292	AD1182	5.6	239	76	hypothetical protein
173	77.5	5.6	293	AH0143	5.6	240	76	hypothetical protein
174	77.5	5.6	296	C95326	5.6	241	76	hypothetical protein
175	77.5	5.6	283	T172289	5.6	242	76	hypothetical protein

249	76	A89153	2	T03836	411	2
250	76	AC0204	2	AB0389	439	2
251	76	958	2	T19112	447	2
252	76	966	2	hypothetical ami	5.4	
253	76	5.5	971	meliobiose carrier	5.4	
254	76	5.5	1052	BDEC	5.4	
255	76	5.5	1074	C86107	469	1
256	75	5.5	1166	meliobiose permease	5.4	
257	75.5	5.4	210	probable amino-acid	5.4	
258	75.5	5.4	237	probable amino-acid	5.4	
259	75.5	5.4	237	probable amino-acid	5.4	
260	75.5	5.4	240	probable amino-acid	5.4	
261	75.5	5.4	252	probable amino-acid	5.4	
262	75.5	5.4	295	probable amino-acid	5.4	
263	75.5	5.4	296	probable amino-acid	5.4	
264	75.5	5.4	297	probable amino-acid	5.4	
265	75.5	5.4	322	probable amino-acid	5.4	
266	75.5	5.4	322	probable amino-acid	5.4	
267	75.5	5.4	338	probable amino-acid	5.4	
273	75.5	5.4	397	probable amino-acid	5.4	
274	75.5	5.4	432	probable amino-acid	5.4	
275	75.5	5.4	432	probable amino-acid	5.4	
276	75.5	5.4	441	probable O-antigen	5.4	
277	75.5	5.4	441	ABC transporter, m	5.4	
278	75.5	5.4	454	ferrichrome ABC tr	5.4	
279	75.5	5.4	454	ferrichrome ABC tr	5.4	
280	75.5	5.4	454	NHC-class II hista	5.4	
281	75.5	5.4	459	adenylate cyclase	5.4	
282	75.5	5.4	476	adenylate cyclase	5.4	
283	75.5	5.4	492	adenylate cyclase	5.4	
284	75.5	5.4	513	adenylate cyclase	5.4	
285	75.5	5.4	532	adenylate cyclase	5.4	
286	75.5	5.4	567	adenylate cyclase	5.4	
287	75	5.4	676	probable aquaporin	5.4	
288	75	5.4	735	probable aquaporin	5.4	
289	75	5.4	740	probable aquaporin	5.4	
290	75	5.4	832	probable aquaporin	5.4	
291	75	5.4	914	probable aquaporin	5.4	
292	75	5.4	932	probable aquaporin	5.4	
293	75	5.4	262	probable aquaporin	5.4	
294	75	5.4	289	probable aquaporin	5.4	
295	75	5.4	291	probable aquaporin	5.4	
296	75	5.4	298	probable aquaporin	5.4	
297	75	5.4	322	probable aquaporin	5.4	
298	75	5.4	322	probable aquaporin	5.4	
299	75	5.4	395	probable aquaporin	5.4	
300	75	5.4	507	probable aquaporin	5.4	
301	75	5.4	1294	probable aquaporin	5.4	
302	75	5.4	599	probable aquaporin	5.4	
303	75	5.4	625	probable aquaporin	5.4	
304	75	5.4	643	probable aquaporin	5.4	
305	75	5.4	917	probable aquaporin	5.4	
306	75	5.4	1056	probable aquaporin	5.4	
307	75	5.4	1294	probable aquaporin	5.4	
308	74.5	5.4	174	probable aquaporin	5.4	
309	74.5	5.4	288	probable aquaporin	5.4	
310	74.5	5.4	293	probable aquaporin	5.4	
311	74.5	5.4	293	probable aquaporin	5.4	
312	74.5	5.4	305	probable aquaporin	5.4	
313	74.5	5.4	311	probable aquaporin	5.4	
314	74.5	5.4	323	probable aquaporin	5.4	
315	74.5	5.4	324	probable aquaporin	5.4	
316	74.5	5.4	325	probable aquaporin	5.4	
317	74.5	5.4	366	probable aquaporin	5.4	
318	74.5	5.4	366	probable aquaporin	5.4	
319	74.5	5.4	367	probable aquaporin	5.4	
320	74.5	5.4	399	probable aquaporin	5.4	
321	74.5	5.4	409	probable aquaporin	5.4	
322	74.5	5.4	439	probable aquaporin	5.4	
323	74.5	5.4	447	probable aquaporin	5.4	
324	74.5	5.4	447	probable aquaporin	5.4	
325	74.5	5.4	469	probable aquaporin	5.4	
326	74.5	5.4	469	probable aquaporin	5.4	
327	74.5	5.4	476	probable aquaporin	5.4	
328	74.5	5.4	544	probable aquaporin	5.4	
329	74.5	5.4	560	probable aquaporin	5.4	
330	74.5	5.4	560	probable aquaporin	5.4	
331	74.5	5.4	726	probable aquaporin	5.4	
332	74.5	5.4	726	probable aquaporin	5.4	
333	74.5	5.4	889	probable aquaporin	5.4	
334	74.5	5.4	953	probable aquaporin	5.4	
335	74.5	5.4	277	probable aquaporin	5.4	
336	74.5	5.4	281	probable aquaporin	5.4	
337	74.5	5.4	296	probable aquaporin	5.4	
338	74.5	5.4	303	probable aquaporin	5.4	
339	74.5	5.4	303	probable aquaporin	5.4	
340	74.5	5.4	322	probable aquaporin	5.4	
341	74.5	5.4	407	probable aquaporin	5.4	
342	74.5	5.4	407	probable aquaporin	5.4	
343	74.5	5.4	446	probable aquaporin	5.4	
344	74.5	5.4	446	probable aquaporin	5.4	
345	74.5	5.4	446	probable aquaporin	5.4	
346	74.5	5.4	446	probable aquaporin	5.4	
347	74.5	5.4	459	probable aquaporin	5.4	
348	74.5	5.4	459	probable aquaporin	5.4	
349	74.5	5.4	459	probable aquaporin	5.4	
350	74.5	5.4	459	probable aquaporin	5.4	
351	74.5	5.4	459	probable aquaporin	5.4	
352	74.5	5.4	459	probable aquaporin	5.4	
353	74.5	5.4	459	probable aquaporin	5.4	
354	74.5	5.4	459	probable aquaporin	5.4	
355	74.5	5.4	508	probable aquaporin	5.4	
356	74.5	5.4	530	probable aquaporin	5.4	
357	74.5	5.4	530	probable aquaporin	5.4	
358	74.5	5.4	532	probable aquaporin	5.4	
359	74.5	5.4	532	probable aquaporin	5.4	
360	74.5	5.4	612	probable aquaporin	5.4	
361	74.5	5.4	740	probable aquaporin	5.4	
362	74.5	5.4	871	probable aquaporin	5.4	
363	74.5	5.4	917	probable aquaporin	5.4	
364	74.5	5.4	947	probable aquaporin	5.4	
365	74.5	5.4	947	probable aquaporin	5.4	
366	74.5	5.4	240	probable aquaporin	5.4	
367	74.5	5.4	240	probable aquaporin	5.4	
368	74.5	5.4	299	probable aquaporin	5.4	
369	74.5	5.4	329	probable aquaporin	5.4	
370	74.5	5.4	337	probable aquaporin	5.4	
371	74.5	5.4	343	probable aquaporin	5.4	
372	74.5	5.4	343	probable aquaporin	5.4	
373	74.5	5.4	372	probable aquaporin	5.4	
374	74.5	5.4	391	probable aquaporin	5.4	
375	74.5	5.4	409	probable aquaporin	5.4	
376	74.5	5.4	423	probable aquaporin	5.4	
377	74.5	5.4	423	probable aquaporin	5.4	
378	74.5	5.4	426	probable aquaporin	5.4	
379	74.5	5.4	433	probable aquaporin	5.4	
380	74.5	5.4	433	probable aquaporin	5.4	
381	74.5	5.4	433	probable aquaporin	5.4	
382	74.5	5.4	476	probable aquaporin	5.4	
383	74.5	5.4	476	probable aquaporin	5.4	
384	74.5	5.4	498	probable aquaporin	5.4	
385	74.5	5.4	507	probable aquaporin	5.4	
386	74.5	5.4	522	probable aquaporin	5.4	
387	74.5	5.4	526	probable aquaporin	5.4	
388	74.5	5.4	526	probable aquaporin	5.4	
389	74.5	5.4	547	probable aquaporin	5.4	
390	74.5	5.4	547	probable aquaporin	5.4	
391	74.5	5.4	592	probable aquaporin	5.4	
392	74.5	5.4	607	probable aquaporin	5.4	
393	74.5	5.4	607	probable aquaporin	5.4	
394	74.5	5.4	630	probable aquaporin	5.4	

395	73.5	674	2	EB2954	conserved hypothetical proteinase [import transporter homologous to NADH2 dehydrogenases]	468	72.5	T13085
396	5.3	699	2	T13730	NADH2 dehydrogenas	469	72.5	741
397	73.5	875	2	H9371	NADH2 dehydrogenas	743	5.2	743
398	73.5	885	2	B69783	NADH2 dehydrogenas	7470	72.5	744
399	73.5	889	2	T20123	hypothetical prote	471	72.5	744
400	73.5	1099	2	A53405	adenylate cyclase	472	72.5	T13757
401	73.5	1128	2	T04922	hypothetical prote	473	72.5	917
402	73.5	1343	2	AF0611	conserved hypothetical prote	474	72.5	C97487
403	73.5	2818	2	B5282	probable membrane protein - importin	475	72.5	AC2705
404	73.5	2820	2	JC5196	mitochondrial Cl- transporter	476	72.5	953
405	73.5	2825	2	T54359	NADH dehydrogenase	477	72.5	S54478
406	73	140	2	C88199	cell division protein	478	72.5	A70634
407	73	193	2	B91170	protein T23G18.2 [fowl]	479	72.5	JC8067
408	73	193	2	B86016	hypothetical prote	480	72.5	H90175
409	73	5.2	261	AC0251	membrane protein	481	72.5	A86216
410	73	5.2	262	F97151	hypothetical prote	482	72	A71234
411	73	5.2	282	H71696	hypothetical prote	483	72	1148
412	73	5.2	283	D89209	probable permease	484	72	AC1024
413	73	5.2	292	C95147	hypothetical membrane protein	485	72	1329
414	73	5.2	294	DB1434	probable membrane protein	486	72	MMVZPD
415	73	5.2	296	A98015	high-affinity zinc ABC transporter	487	72	S62047
416	73	5.2	301	AH2064	ABC transported MD	488	72	F75166
417	73	5.2	311	T33436	hypothetical prote	489	72	A71165
423	73	5.2	364	D95959	probable permease	490	72	257
424	73	5.2	364	AD1556	conserved hypothetical protein	491	72	AC1024
425	73	5.2	384	H97735	NADH2 dehydrogenas	492	72	1329
426	73	5.2	399	AT0396	probable sugar transporter	493	72	2
427	73	5.2	401	T4929	hypothetical prote	494	72	260
428	73	5.2	436	S71639	exopolysaccharide	495	72	D98058
429	73	5.2	437	D86633	hypothetical prote	496	72	T23066
430	73	5.2	453	AB1370	conserved hypothetical protein	497	72	B83778
431	73	5.2	456	T05964	hypothetical prote	498	72	E86761
432	73	5.2	470	B86118	probable sugar transporter	499	72	T23244
433	73	5.2	470	B91277	transport of D-alanine	500	72	A5573
434	73	5.2	470	S56333	D-serine/D-alanine	501	72	AF3044
435	73	5.2	495	S25942	amino acid permeas	502	72	C84246
436	73	5.2	507	AD1556	conserved hypothetical protein	503	72	C82943
437	73	5.2	574	H97735	probable low-affin	504	72	F98241
438	73	5.2	633	T19389	hypothetical prote	505	72	T34372
439	73	5.2	639	G88839	D-serine/D-alanine	506	72	F90916
440	73	5.2	700	T13668	D-serine/D-alanine	507	72	T24076
441	72.5	732	2	T14231	NADH2 dehydrogenas	508	72	C85765
442	72.5	732	2	T27121	hypothetical prote	509	72	B84129
443	72.5	271	2	T11704	probable CMCase-AC	510	72	C82432
444	72.5	271	2	RGBY12	probable dipeptidyl	511	72	C82410
445	72.5	284	2	GNWHLB	genome polyprotein	512	72	C75107
446	72.5	286	2	3898	hypothetical prote	513	72	F64915
447	72.5	297	2	F82039	protein C10C6.5 [i]	514	72	AE0094
448	72.5	297	2	A99015	NADH2 dehydrogenas	515	72	H71732
449	72.5	330	2	AF0198	hypothetical prote	516	72	H69804
450	72.5	347	2	D95902	probable CMCase-AC	517	72	T17022
451	72.5	375	2	AD2201	probable dipeptidyl	518	72	B71695
452	72.5	421	2	T22669	cytochrome C oxidase	519	72	AD1897
453	72.5	434	2	D65132	ribonuclease BN VC	520	72	C83976
454	72.5	459	2	B90523	probable membrane	521	72	T51836
455	72.5	459	2	T19110	probable sugar ABC	522	72	AG2707
456	72.5	461	2	G85059	hypothetical prote	523	72	H97489
457	72.5	461	2	S75711	NADH2 dehydrogenas	524	72	AC2313
458	72.5	491	2	H83979	Na+/H+-exchanging	525	72	T12565
459	72.5	494	1	F69355	hypothetical prote	526	72	T12160
460	72.5	498	2	B89832	NADH2 dehydrogenas	527	72	S55312
461	72.5	523	2	A11970	hypothetical prote	528	72	AG2164
462	72.5	615	2	S77084	ABC-type transporter	529	72	T12161
463	72.5	646	2	B70001	NADH2 dehydrogenas	530	72	T13763
464	72.5	682	2	T12715	NADH2 dehydrogenas	531	72	2
465	72.5	684	2	T13491	NADH2 dehydrogenas	532	72	T13793
466	72.5	704	2	T13665	NADH2 dehydrogenas	533	72	S62464
467	72.5	736	2	T12716	NADH2 dehydrogenas	534	72	T12160

5.1	541	71.5	295	2	AB0462	en-glycerol-3-phos	probable transport	468	2	D83625	
5.1	542	71.5	296	2	T32277	hypothetical prote	5.1	71	614	5.1	
5.1	543	71.5	308	2	H70767	MDR-type permease	5.1	71	615	469	
5.1	544	71.5	323	2	G84003	proline symporter	2	478	478	A88075	
5.1	545	71.5	324	2	F81048	NADH2 dehydrogenas	2	492	2	D5188	
5.1	546	71.5	337	2	F82214	nicotinic acetylch	2	498	2	H81796	
5.1	547	71.5	341	2	F82272	nicotinic acetylch	1	502	1	ACTUAT	
5.1	548	71.5	348	2	A82322	alpha 7 neuronal n	2	502	2	G02259	
5.1	549	71.5	349	2	T31856	nicotinic acetylch	2	502	2	A57175	
5.1	550	71.5	373	2	A98094	beta-lactamase receptor	2	502	2	T01378	
5.1	551	71.5	373	2	E85939	beta-lactamase ind	2	509	2	A82840	
5.1	552	71.5	373	2	D71142	iron(III) ABC tran	2	541	2	DB8302	
5.1	553	71.5	382	2	A85014	hypothetical prote	2	541	2	T24671	
5.1	554	71.5	391	2	A55119	probable amino aci	2	555	2	T00477	
5.1	555	71.5	406	2	C86904	ABC transporter (A	2	559	2	AB1414	
5.1	556	71.5	418	2	H97763	probable ABC trans	2	562	2	A10559	
5.1	557	71.5	432	2	D95369	cellular Hep70 hom	2	562	2	T01378	
5.1	564	71.5	445	2	T20190	bifur deprivatio	2	563	2	A49804	
5.1	565	71.5	470	2	A69751	NADH2 dehydrogenas	2	564	2	S74936	
5.1	566	71.5	470	2	C70534	NADH2 dehydrogenas	2	565	2	T12151	
5.1	567	71.5	477	2	F86670	NADH2 dehydrogenas	2	566	2	T12128	
5.1	568	71.5	497	2	G81598	NADH2 dehydrogenas	2	567	2	T12128	
5.1	569	71.5	506	2	F88934	related to PAN2 pr	2	568	2	A10559	
5.1	570	71.5	512	2	S75887	hypothetical prote	2	569	2	T12560	
5.1	571	71.5	519	2	S77555	hypothetical prote	2	570	2	T12648	
5.1	572	71.5	519	2	H72067	hypothetical prote	2	571	2	T12138	
5.1	573	71.5	532	2	S59087	hypothetical prote	2	572	2	T13237	
5.1	574	71.5	532	2	S66087	membrane glycoprot	2	573	2	A36337	
5.1	575	71.5	533	2	H69326	related to PAN2 pr	2	574	2	T13249	
5.1	576	71.5	534	2	C87023	hypothetical prote	2	575	2	A13582	
5.1	577	71.5	539	2	S77555	hypothetical prote	2	576	2	T20548	
5.1	578	71.5	551	2	B98202	hypothetical prote	2	577	2	T29414	
5.1	579	71.5	663	2	AG2636	hypothetical prote	2	578	2	T04051	
5.1	580	71.5	663	2	G97478	c-type cytochrome	2	579	2	T04051	
5.1	581	71.5	665	2	B96668	c-type cytochrome	2	580	2	S76538	
5.1	582	71.5	672	2	AF3084	probable acyl-CoA	2	581	2	CS48115	
5.1	583	71.5	672	2	T12642	conserved hypothet	2	582	2	F75067	
5.1	584	71.5	741	2	T12701	probable cell divi	2	583	2	A13582	
5.1	585	71.5	746	2	T13678	c-type cytochrome	2	584	2	T20548	
5.1	586	71.5	756	2	T04187	cytochrome c-type	2	585	2	T29414	
5.1	587	71.5	756	2	F97186	cytochrome c-type	2	586	2	T04051	
5.1	588	71.5	760	2	T23999	probable acyl-CoA	2	587	2	T04051	
5.1	589	71.5	854	2	D8234	conserved hypothet	2	588	2	S76538	
5.1	590	71.5	1067	2	AB0260	probable phage hos	2	589	2	T04051	
5.1	591	71	1679	2	T50091	yeast Rcm29 cell w	2	590	2	S76538	
5.1	592	71	200	1	F45456	NADH2 dehydrogenas	2	591	2	T12435	
5.1	593	71	5.1	228	2	AE2541	probable membrane	2	592	2	D87209
5.1	594	71	5.1	272	2	A64137	ferrichrome ABC tr	2	593	2	C81962
5.1	595	71	5.1	297	2	AD2318	probable inner mem	2	594	2	T02451
5.1	596	71	5.1	343	2	B86740	transmembrane prot	2	595	2	T02451
5.1	597	71	5.1	397	2	C95221	probable sodium de	2	596	2	T02451
5.1	598	71	5.1	397	2	AB2931	hypothetical prote	2	597	2	T02451
5.1	599	71	5.1	397	2	T00098	probable iron-side	2	598	2	T02451
5.1	600	71	5.1	397	2	B98085	probable membrane	2	599	2	T02451
5.1	601	71	5.1	397	2	T30982	hypothetical prote	2	600	2	T02451
5.1	602	71	5.1	397	2	A64143	probable O-antigen	2	601	2	T02451
5.1	603	71	5.1	397	2	E64143	probable CAXX pro	2	602	2	T02451
5.1	604	71	5.1	397	2	B64143	SCA protein - Sta	2	603	2	T15799
5.1	605	71	5.1	397	2	B64143	transmembrane prot	2	604	2	S39978
5.1	606	71	5.1	397	2	C95221	glycine betaine tr	2	605	2	AC1499
5.1	607	71	5.1	397	2	B64143	probable O-antigen	2	606	2	D71058
5.1	608	71	5.1	397	2	B64143	probable phosphate	2	607	2	A67779
5.1	609	71	5.1	448	2	T30982	amino acid transpo	2	608	2	T02451
5.1	610	71	5.1	458	2	AF0331	probable sodium pr	2	609	2	T02451
5.1	611	71	5.1	461	2	S6023	cytochrome-c oxi	2	610	2	C82955
5.1	612	71	5.1	466	2	B90046	cytochrome-c oxi	2	611	2	JT0974
5.1	613	71	5.1	468	2	164182	Na+/H+ -exchang	2	612	2	F84223

687	70.5	5.1	674	2	AC1913	760	70	GNNYA9
688	70.5	5.1	683	2	T12158	69.5	5.0	202
689	70.5	5.1	704	2	T12581	69.5	5.0	210
690	70.5	5.1	718	2	S48726	69.5	5.0	210
691	70.5	5.1	733	2	T12213	69.5	5.0	215
692	70.5	5.1	737	2	T13504	69.5	5.0	222
693	70.5	5.1	738	2	C95336	69.5	5.0	224
694	70.5	5.1	740	1	DENTN5	69.5	5.0	256
695	70.5	5.1	741	2	T12610	69.5	5.0	265
696	70.5	5.1	741	2	T12702	69.5	5.0	268
697	70.5	5.1	741	2	T13233	69.5	5.0	285
704	70	5.0	98	2	T12099	770	5.0	1
705	70	5.0	160	2	F72322	771	5.0	C32804
706	70	5.0	169	2	AB2739	772	5.0	AE1488
707	70	5.0	209	2	H97519	773	5.0	F87075
708	70	5.0	240	1	QQB63	774	5.0	A70417
709	70	5.0	2143	2	G95695	775	5.0	Staphylococcus xylophilus
710	70	5.0	250	2	A90527	776	5.0	membrane transport
711	70	5.0	251	2	C91020	777	5.0	conserved hypothet
712	70	5.0	254	2	AH0575	778	5.0	hypothetical prote
713	70	5.0	273	2	A72378	779	5.0	NADH2 dehydrogenas
714	70	5.0	282	2	A99205	780	5.0	hypothetical prote
715	70	5.0	287	2	T12440	781	5.0	NADH2 dehydrogenas
716	70	5.0	320	2	T20176	782	5.0	hypothetical prote
717	70	5.0	325	2	C98135	783	5.0	NADH2 dehydrogenas
718	70	5.0	325	2	AH3152	784	5.0	hypothetical prote
719	70	5.0	344	2	AE3228	785	5.0	hypothetical prote
720	70	5.0	344	2	SS1948	786	5.0	hypothetical prote
721	70	5.0	345	2	H95381	787	5.0	hypothetical prote
722	70	5.0	397	2	AF2016	788	5.0	hypothetical prote
723	70	5.0	413	2	H81659	789	5.0	hypothetical prote
724	70	5.0	427	2	S7444	790	5.0	hypothetical prote
725	70	5.0	442	2	E85664	791	5.0	hypothetical prote
726	70	5.0	443	2	F91228	792	5.0	hypothetical prote
727	70	5.0	443	2	H90534	793	5.0	hypothetical prote
728	70	5.0	456	2	F97515	794	5.0	hypothetical prote
729	70	5.0	458	2	A37610	795	5.0	hypothetical prote
730	70	5.0	459	2	T1110	796	5.0	hypothetical prote
731	70	5.0	459	2	S28025	797	5.0	probable transport
732	70	5.0	467	2	E85485	798	5.0	probable transport
733	70	5.0	503	2	AB2734	799	5.0	probable permease
734	70	5.0	600	2	D97515	800	5.0	NADH2 dehydrogenase
735	70	5.0	519	2	F84222	801	5.0	magnesium transpor
736	70	5.0	522	2	B83987	802	5.0	alpha-2B-adrenergic
737	70	5.0	539	2	E97025	803	5.0	probable transport
738	70	5.0	539	2	S67049	804	5.0	light harvesting C
739	70	5.0	576	2	T12194	805	5.0	probable transport
740	70	5.0	600	2	T32333	806	5.0	NADH2 dehydrogenase
741	70	5.0	614	2	B84449	807	5.0	probable permease
742	70	5.0	658	2	B86559	808	5.0	NADH2 dehydrogenase
743	70	5.0	658	2	D72026	809	5.0	probable membrane
744	70	5.0	670	2	JQ1447	810	5.0	probable membrane
750	70	5.0	670	2	C81515	811	5.0	probable membrane
745	70	5.0	683	2	T12670	812	5.0	probable membrane
746	70	5.0	688	2	T12556	813	5.0	probable membrane
747	70	5.0	698	2	T13702	814	5.0	probable membrane
748	70	5.0	700	2	T13702	815	5.0	probable membrane
749	70	5.0	705	2	T13494	816	5.0	probable membrane
755	70	5.0	860	2	AB2044	817	5.0	cation transportin
756	70	5.0	1018	2	T19693	823	5.0	NADH2 dehydrogenase
757	70	5.0	1070	2	B86922	824	5.0	probable membrane
758	70	5.0	1155	2	B71720	830	5.0	probable membrane
759	70	5.0	1155	2	S72458	831	5.0	probable membrane

833	69.5	741	2	T13372	NADH2 dehydrogenas	906	69	670	1
834	5.0	744	2	T13682	NADH2 dehydrogenas	907	69	5.0	670
835	69.5	747	2	E9049	NADH2 dehydrogenas	908	69	5.0	5.0
836	69.5	747	2	A85894	probable cytochrom	909	69	5.0	684
837	69.5	809	1	SYBQQT	probable cytochrome -RNA lig	910	69	5.0	691
838	69.5	970	2	A11605	potassium efflux s	911	69	5.0	691
839	69.5	1302	2	B41249	multidrug resistant	912	69	5.0	692
840	69.5	1645	2	T31339	carbamoyl-phosphat	912	69	5.0	702
841	69.5	1827	2	S43694	cut1 protein - fis	913	69	5.0	724
842	69.5	1828	2	T41455	cut1 protein - fis	914	69	5.0	737
843	69	5.0	254	CB8315	hypothetical prote	915	69	5.0	737
844	69	5.0	260	AG0434	probable membrane	916	69	5.0	741
845	69	5.0	281	D64426	hypothetical prote	917	69	5.0	741
851	69	5.0	288	H72092	cytochrome-c	918	68.5	4.9	745
852	69	5.0	288	G85229	probable membrane	919	68.5	4.9	745
853	69	5.0	290	T03260	TEGT protein - rat	920	68.5	4.9	745
854	69	5.0	292	DB1575	hypothetical prote	921	68.5	4.9	745
855	69	5.0	296	BVBCPT	phosphate transpor	922	68.5	4.9	745
856	69	5.0	296	F91211	probable membrane	923	68.5	4.9	745
857	69	5.0	296	F88057	hypothetical prote	924	68.5	4.9	745
858	69	5.0	299	T03960	probable membrane	925	68.5	4.9	745
859	69	5.0	305	F70030	conserved hypothet	926	68.5	4.9	745
860	69	5.0	308	DB1575	phosphatidate cyti	927	68.5	4.9	745
861	69	5.0	308	H72062	phosphate transpor	928	68.5	4.9	745
862	69	5.0	313	H71341	probable membrane	929	68.5	4.9	745
863	69	5.0	347	T29415	hypothetical prote	930	68.5	4.9	745
864	69	5.0	364	D98973	spore germination	931	68.5	4.9	745
865	69	5.0	369	F69478	NADH2 dehydrogenas	932	68.5	4.9	745
866	69	5.0	387	E88679	multidrug-efflux t	933	68.5	4.9	745
867	69	5.0	389	T51355	membrane protein [934	68.5	4.9	745
868	69	5.0	391	AB1285	transmembrane tran	935	68.5	4.9	745
869	69	5.0	396	F83130	probable MFS trans	936	68.5	4.9	745
870	69	5.0	397	B81223	conserved hypothet	937	68.5	4.9	745
871	69	5.0	397	B81994	probable transmemb	938	68.5	4.9	745
872	69	5.0	411	F97088	sugar-proton sympo	939	68.5	4.9	745
873	69	5.0	416	C81324	ubiquinol-cytochro	940	68.5	4.9	745
874	69	5.0	429	A10792	probable transport	941	68.5	4.9	745
875	69	5.0	431	A83380	hypothetical prote	942	68.5	4.9	745
876	69	5.0	432	A85087	hypothetical prote	943	68.5	4.9	745
877	69	5.0	443	B61725	yaaU protein - Esc	944	68.5	4.9	745
878	69	5.0	449	AB1781	PTS system galacti	945	68.5	4.9	745
879	69	5.0	451	C81781	probable integral	946	68.5	4.9	745
880	69	5.0	451	A81206	sugar transporter,	947	68.5	4.9	745
881	69	5.0	455	C90619	NADH dehydrogenase	948	68.5	4.9	745
882	69	5.0	458	B96543	integral membrane	949	68.5	4.9	745
883	69	5.0	462	D86314	probable permease	950	68.5	4.9	745
884	69	5.0	464	C40630	transport protein	951	68.5	4.9	745
885	69	5.0	473	T03611	GDP-mannose pyroph	952	68.5	4.9	745
886	69	5.0	478	T29174	cyclin, B-type - C	953	68.5	4.9	745
887	69	5.0	482	A81206	hypothetical prote	954	68.5	4.9	745
888	69	5.0	483	A81352	probable NADH dehy	955	68.5	4.9	745
889	69	5.0	487	S40820	probable permease	956	68.5	4.9	745
890	69	5.0	488	I	cytochrome-c	957	68.5	4.9	745
891	69	5.0	522	A98231	oxida	958	68.5	4.9	745
892	69	5.0	528	T34941	probable thiol-dis	959	68.5	4.9	745
893	69	5.0	544	S03609	NADH2 dehydrogenas	960	68.5	4.9	745
900	69	5.0	548	A43740	hypothetical prote	961	68.5	4.9	745
901	69	5.0	559	D86978	probable NADH dehy	962	68.5	4.9	745
902	69	5.0	565	G82282	probable NADH dehy	963	68.5	4.9	745
903	69	5.0	605	A95205	succinoglycan bios	964	68.5	4.9	745
904	69	5.0	605	A99705	probable Na+/H+ an	965	68.5	4.9	745
905	69	5.0	642	T33262	cytochrome-c oxida	966	68.5	4.9	745
				C97087	DG42 protein - Afr	973	68.5	4.9	745
					vird4 protein [imp	974	68.5	4.9	745
					conserved hypothet	975	68.5	4.9	745
					hypothetical prote	976	68.5	4.9	745
					hypothetical prote	977	68.5	4.9	745
					probable permease	978	68.5	4.9	745

979	68.5	820	2	D71471	1052	68	4.9	S76449
980	68.5	827	2	A89277	1053	68	4.9	S33442
981	68.5	870	2	A89201	1054	68	4.9	F72453
982	68.5	874	2	JQ0883	1055	68	4.9	C87083
983	68.5	881	2	B97277	1056	68	4.9	T45096
984	68.5	881	2	B97557	1057	68	4.9	T18214
985	68.5	912	2	T21659	1058	68	4.9	T51622
986	68.5	960	2	A82142	1059	68	4.9	hypothetical prote
987	68.5	1081	2	T52028	1060	67.5	4.8	probable ABC trans
988	68.5	1084	2	T08383	1061	67.5	4.8	hypothetical prote
989	68.5	1394	2	S66376	1062	67.5	4.8	hypothetical prote
990	68.5	1504	2	A33602	1063	67.5	4.8	Streptococcus agal
991	68	148	2	S74589	1064	67.5	4.8	hypothetical prote
992	68	183	2	T49855	1065	67.5	4.8	probable ABC trans
993	68	214	2	G83882	1066	67.5	4.8	probable permease
994	68	215	2	S16564	1067	67.5	4.8	probable sugar prot
995	68	237	2	H86841	1068	67.5	4.8	hypothetical prote
996	68	241	2	T33804	1069	67.5	4.8	hypothetical prote
1003	68	286	2	D83914	1070	67.5	4.8	NADPH2:quinone red
1004	68	296	2	A70529	1071	67.5	4.8	ABC transporter, m
1005	68	304	2	E70438	1072	67.5	4.8	probable membrane
1006	68	312	2	AD014	1073	67.5	4.8	probable membrane
1007	68	316	2	E82716	1074	67.5	4.8	probable membrane
1008	68	316	2	AD0648	1075	67.5	4.8	hypothetical prote
1009	68	329	2	P98334	1076	67.5	4.8	hypothetical prote
1010	68	335	2	S44635	1077	67.5	4.8	probable membrane
1011	68	353	2	T06515	1078	67.5	4.8	hypothetical prote
1012	68	357	2	C97744	1079	67.5	4.8	probable membrane
1013	68	358.	2	T38914	1080	67.5	4.8	probable membrane
1014	68	396	2	AF0677	1081	67.5	4.8	probable membrane
1015	68	396	2	A91019	1082	67.5	4.8	probable membrane
1016	68	396	2	C85863	1083	67.5	4.8	probable membrane
1017	68	397	2	G90013	1084	67.5	4.8	probable membrane
1018	68	408	2	AC1373	1085	67.5	4.8	probable membrane
1019	68	417	2	E82936	1086	67.5	4.8	probable membrane
1020	68	417	1	F64614	1087	67.5	4.8	probable membrane
1021	68	442	2	HB1402	1088	67.5	4.8	probable membrane
1022	68	448	2	G70172	1089	67.5	4.8	probable membrane
1023	68	461	2	H82186	1090	67.5	4.8	probable membrane
1024	68	469	2	C6928	1091	67.5	4.8	probable membrane
1025	68	476	2	D83600	1092	67.5	4.8	probable membrane
1026	68	495	2	T24115	1093	67.5	4.8	probable membrane
1027	68	495	1	OXASN4	1094	67.5	4.8	probable membrane
1032	68	521	2	B64181	1095	67.5	4.8	probable membrane
1033	68	523	2	T12198	1096	67.5	4.8	probable membrane
1034	68	534	2	S64593	1097	67.5	4.8	probable membrane
1035	68	537	2	AH1640	1098	67.5	4.8	probable membrane
1036	68	550	2	B97747	1099	67.5	4.8	probable membrane
1031	68	551	2	G90399	1100	67.5	4.8	probable membrane
1038	68	592	2	E70488	1105	67.5	4.8	probable membrane
1039	68	593	2	S26636	1106	67.5	4.8	probable membrane
1040	68	600	2	C69371	1113	67.5	4.8	probable membrane
1041	68	602	2	T13679	1114	67.5	4.8	probable membrane
1042	68	617	2	F82744	1115	67.5	4.8	probable membrane
1043	68	633	2	C83742	1116	67.5	4.8	probable membrane
1044	68	633	2	B64181	1117	67.5	4.8	probable membrane
1045	68	638	2	JH0673	1118	67.5	4.8	probable membrane
1046	68	683	2	T12295	1119	67.5	4.8	probable membrane
1047	68	688	2	T13278	1120	67.5	4.8	probable membrane
1048	68	689	2	T13762	1121	67.5	4.8	probable membrane
1049	68	705	2	T12152	1122	67.5	4.8	probable membrane
1050	68	709	2	A97218	1123	67.5	4.8	probable membrane
1051	68	811	2	T36581	1124	67.5	4.8	probable membrane

1125	4.8	637	2	JH0674	L-proline transpor	1198	4.8	406	2	H89006	
1126	67.5	4.8	645	2	T12159	O-antigen polymera	1199	4.8	407	2	A0706
1127	67.5	4.8	645	2	A75380	O-antigen polymera	1200	4.8	407	2	A33672
1128	67.5	4.8	659	2	T33557	NADH2 dehydrogenas	1201	4.8	409	2	C82644
1129	67.5	4.8	690	2	D75487	hypothetical prote	1202	4.8	411	2	S61245
1130	67.5	4.8	690	2	T12169	v-type ATP synthas	1203	4.8	416	2	JN0720
1131	67.5	4.8	703	2	T13074	NADH2 dehydrogenas	1204	4.8	417	2	H83708
1132	67.5	4.8	741	2	T13404	NADH2 dehydrogenas	1205	4.8	421	2	AF2382
1133	67.5	4.8	741	2	T13760	NADH2 dehydrogenas	1206	4.8	423	2	EB82611
1134	67.5	4.8	741	2	T13776	NADH2 dehydrogenas	1207	4.8	430	2	S74039
1135	67.5	4.8	741	2	T12762	NADH2 dehydrogenas	1208	4.8	446	2	AC3349
1142	67.5	4.8	744	2	T12694	NADH2 dehydrogenas	1209	4.8	453	2	A43765
1143	67.5	4.8	744	2	T12611	NADH2 dehydrogenas	1210	4.8	453	2	T30985
1137	67.5	4.8	801	2	A89862	Na+/H+ antipoter	1211	4.8	456	2	A1778
1138	67.5	4.8	812	2	T19446	hypothetical prote	1212	4.8	458	2	H71657
1139	67.5	4.8	900	2	D97351	trimethylamine-N-O	1213	4.8	459	1	DNHUN4
1140	67.5	4.8	920	2	G82168	ZC21.2 protein - C	1214	4.8	461	2	H97568
1141	67.5	4.8	823	2	S44873	probable integral	1215	4.8	462	2	T34365
1142	67.5	4.8	823	2	B81282	calcium-transport	1216	4.8	468	2	AD0521
1143	67.5	4.8	890	2	H69877	sensor protein Kdp	1217	4.8	469	2	T35670
1144	67.5	4.8	1517	2	F85985	cytochrome c bioge	1218	4.8	470	2	T26602
1145	67.5	4.8	936	2	B64567	hypothetical prote	1219	4.8	473	2	AG0612
1146	67.5	4.8	952	2	T32836	trascriptural repa	1220	4.8	477	2	S71323
1147	67.5	4.8	1199	2	S76549	structural polypro	1221	4.8	485	2	C70488
1148	67.5	4.8	1247	1	VHWN2	glutamate synthase	1222	4.8	491	2	GE5251
1149	67.5	4.8	1517	2	F65112	glutamate synthase	1223	4.8	494	2	AC0133
1150	67.5	4.8	1517	2	D97351	conjugal transfer	1224	4.8	511	2	H90439
1151	67.5	4.8	1517	2	C91140	crtB protein limpo	1225	4.8	516	2	T33269
1152	67.5	4.8	1704	2	T42249	ABC-binding cassette	1226	4.8	517	2	AC2070
1153	67.5	4.8	1767	2	S60124	transport protein	1227	4.8	517	2	E83147
1154	67.5	4.8	1778	2	AF1116	internalin protein	1228	4.8	522	2	P862215
1155	67.5	4.8	2701	2	S17736	inositol-trisphosp	1229	4.8	527	2	T49241
1156	67	4.8	290	2	E82861	conjugal transfer	1230	4.8	537	2	D70478
1157	67	4.8	109	2	C98018	crtB protein limpo	1231	4.8	546	2	AB0571
1158	67	4.8	1704	2	T42249	hypothetical prote	1232	4.8	557	2	T44520
1159	67	4.8	180	2	C86290	membrane protein I	1233	4.8	557	2	S56168
1160	67	4.8	187	2	A95143	conserved hypothet	1234	4.8	557	2	GE5096
1161	67	4.8	187	2	G98010	conjugal transfer	1235	4.8	574	2	T41068
1162	67	4.8	226	2	S57521	crtB protein limpo	1236	4.8	574	2	T34208
1163	67	4.8	232	1	G64591	conserved hypothet	1237	4.8	584	2	B82810
1164	67	4.8	259	2	S59152	cyclochrome-c oxida	1238	4.8	585	2	T19245
1165	67	4.8	260	2	A91138	hypothetical prote	1239	4.8	605	2	A16361
1166	67	4.8	260	2	D65110	membrane protein I	1240	4.8	625	2	T33792
1167	67	4.8	260	2	D85983	hypothetical prote	1241	4.8	625	2	AD2251
1168	67	4.8	261	2	T11826	cyclochrome-c oxida	1242	4.8	640	2	D90174
1169	67	4.8	265	2	T05668	conserved hypothet	1243	4.8	644	2	S44478
1170	67	4.8	268	2	A99349	cyclochrome-c oxida	1244	4.8	653	2	C55022
1171	67	4.8	278	2	A84244	hypothetical prote	1245	4.8	659	2	T12586
1172	67	4.8	287	2	A84244	membrane glycoprot	1246	4.8	698	2	T12568
1173	67	4.8	287	2	S23396	hypothetical prote	1247	4.8	698	2	S76532
1174	67	4.8	288	2	I78556	hypothetical prote	1248	4.8	700	2	A44257
1175	67	4.8	291	2	S48977	conserved hypothet	1249	4.8	707	2	G86894
1176	67	4.8	293	2	D86065	hypothetical prote	1250	4.8	741	1	S34218
1177	67	4.8	293	2	B91219	baicatin resistance	1251	4.8	741	2	JC6312
1178	67	4.8	308	2	H65182	cyclochrome-c oxida	1252	4.8	788	2	A8066
1179	67	4.8	313	2	H64409	hypothetical prote	1253	4.8	878	2	S73015
1180	67	4.8	313	2	T24294	hypothetical prote	1254	4.8	918	2	A44257
1181	67	4.8	313	2	C95247	conserved hypothet	1255	4.8	970	2	F64230
1182	67	4.8	313	2	H98111	hypothetical prote	1255	4.8	1001	2	T13807
1183	67	4.8	314	2	F81699	peptide ABC transp	1256	4.8	1218	2	S38182
1184	67	4.8	323	2	AB0427	octaprenyl-diphosp	1257	4.8	1440	2	A95058
1185	67	4.8	328	2	D72566	hypothetical prote	1258	4.8	1457	1	B87385
1186	67	4.8	349	2	AD0290	probable membrane	1259	4.8	1489	2	S73015
1187	67	4.8	354	2	C82038	nitrogen regulatio	1260	4.8	1559	2	A12348
1188	67	4.8	356	2	B84749	hypothetical prote	1261	4.8	1655	2	F88559
1189	67	4.8	364	2	T45253	probable antiporte	1262	4.8	1783	2	S47307
1190	67	4.8	364	2	T24418	hypothetical prote	1263	4.8	1900	2	AB1922
1191	67	4.8	367	2	S23349	octaprenyl-diphosp	1264	4.8	1975	2	D81327
1192	67	4.8	371	2	D9790	cell division prot	1265	4.8	205	2	A87460
1193	67	4.8	377	2	B71639	hypothetical prote	1266	4.8	205	2	AB7460
1194	67	4.8	388	2	B64459	Na+/H+ exchangin	1267	4.8	217	2	B69396
1195	67	4.8	394	2	AH0020	conserved integral	1268	4.8	245	2	F1887
1196	67	4.8	397	2	B70763	probable membrane	1269	4.8	256	2	G82804
1197	67	4.8	401	2	H82175	multidrug resistan	1270	4.8	258	2	A69830

1271	2	I64249	1344	4.8	744	2	T13063
1272	2	A86889	1345	66.5	744	2	T13048
1273	4.8	B67226	1346	66.5	746	2	T01536
1274	66.5	4.8	1347	66.5	755	2	T20950
1275	66.5	4.8	1348	66.5	759	2	D70422
1276	66.5	4.8	1349	66.5	4.8	2	G90477
1277	66.5	4.8	1350	66.5	4.8	2	T16621
1278	66.5	4.8	1351	66.5	812	2	T41978
1279	66.5	4.8	1352	66.5	820	2	C82750
1280	66.5	4.8	1353	66.5	860	2	H+-exporting ATPase
1281	66.5	4.8	1354	66.5	919	2	Glutamate receptor - kainate receptor - olfactory receptor channel
1282	66.5	4.8	1355	66.5	919	2	B. subtilis YueB P
1283	66.5	4.8	1356	66.5	937	2	probable membrane protein Bc212.5 [i]
1284	66.5	4.8	1357	66.5	957	2	hypothetical prote
1285	66.5	4.8	1358	66.5	999	2	conserved membrane protein
1286	66.5	4.8	1359	66.5	1002	2	probable ABC transporter
1287	66.5	4.8	1360	66.5	1010	1	ATP-binding cassette
1288	66.5	4.8	1361	66.5	1049	2	hypothetical prote
1289	66.5	4.8	1362	66.5	1049	2	hypothetical prote
1290	66.5	4.8	1363	66.5	1068	2	probable cellulose
1291	66.5	4.8	1364	66.5	1068	2	autolysin [imported membrane protein]
1292	66.5	4.8	1365	66.5	1088	2	probable membrane protein
1293	66.5	4.8	1366	66.5	1248	2	probable multidrug
1294	66.5	4.8	1367	66.5	1248	2	probable membrane protein
1295	66.5	4.8	1368	66.5	1248	2	probable olfactory receptor
1296	66.5	4.8	1369	66.5	1248	2	amino acid transporter - Pse
1297	66.5	4.8	1370	66.5	1704	2	hypothetical prote
1298	66.5	4.8	1371	66.5	1704	2	alpha-crystallin C
1299	66.5	4.8	1372	66.5	1704	2	hypothetical prote
1300	66.5	4.8	1373	66.5	1704	2	hypothetical prote
1301	66.5	4.8	1374	66.5	1705	2	hypothetical prote
1302	66.5	4.8	1375	66.5	1705	2	hypothetical prote
1303	66.5	4.8	1376	66.5	1705	2	hypothetical prote
1304	66.5	4.8	1377	66.5	1705	2	hypothetical prote
1305	66.5	4.8	1378	66.5	1705	2	hypothetical prote
1310	66.5	4.8	1379	66.5	1705	2	hypothetical prote
1311	66.5	4.8	1380	66.5	1705	2	hypothetical prote
1312	66.5	4.8	1381	66.5	1705	2	hypothetical prote
1313	66.5	4.8	1382	66.5	1705	2	hypothetical prote
1314	66.5	4.8	1383	66.5	1705	2	hypothetical prote
1315	66.5	4.8	1384	66.5	1705	2	hypothetical prote
1316	66.5	4.8	1385	66.5	1705	2	hypothetical prote
1317	66.5	4.8	1386	66.5	1705	2	hypothetical prote
1318	66.5	4.8	1387	66.5	1705	2	hypothetical prote
1319	66.5	4.8	1388	66.5	1705	2	hypothetical prote
1320	66.5	4.8	1389	66.5	1705	2	hypothetical prote
1321	66.5	4.8	1390	66.5	1705	2	hypothetical prote
1322	66.5	4.8	1391	66.5	1705	2	hypothetical prote
1323	66.5	4.8	1392	66.5	1705	2	hypothetical prote
1324	66.5	4.8	1393	66.5	1705	2	hypothetical prote
1325	66.5	4.8	1394	66.5	1705	2	hypothetical prote
1326	66.5	4.8	1395	66.5	1705	2	hypothetical prote
1327	66.5	4.8	1396	66.5	1705	2	hypothetical prote
1328	66.5	4.8	1397	66.5	1705	2	hypothetical prote
1329	66.5	4.8	1398	66.5	1705	2	hypothetical prote
1330	66.5	4.8	1399	66.5	1705	2	hypothetical prote
1331	66.5	4.8	1400	66.5	1705	2	hypothetical prote
1332	66.5	4.8	1401	66.5	1705	2	hypothetical prote
1333	66.5	4.8	1402	66.5	1705	2	hypothetical prote
1334	66.5	4.8	1403	66.5	1705	2	hypothetical prote
1335	66.5	4.8	1404	66.5	1705	2	hypothetical prote
1336	66.5	4.8	1405	66.5	1705	2	hypothetical prote
1337	66.5	4.8	1406	66.5	1705	2	hypothetical prote
1338	66.5	4.8	1407	66.5	1705	2	hypothetical prote
1339	66.5	4.8	1408	66.5	1705	2	hypothetical prote
1340	66.5	4.8	1409	66.5	1705	2	hypothetical prote
1341	66.5	4.8	1410	66.5	1705	2	hypothetical prote
1342	66.5	4.8	1411	66.5	1705	2	hypothetical prote
1343	66.5	4.8	1412	66.5	1705	2	hypothetical prote

C;Genetics: CESP:C33A11.2
 A;Gene: C33A11.2
 A;Map position: X
 A;Intron Position: 26/1; 117/3; 177/1; 208/3
 C;Superfamily: Caenorhabditis elegans hypothetical protein C36F7.4b
 Query Match 20.7%; Score 288; DB 2; Length 271;
 Best Local Similarity 30.9%; Pred. No. 1e-17;
 Matches 71; Conservative 43; Mismatches 104; Indels 12; Gaps 6;
 Qy 14 ALVWTSSAFAFSYTATVLHHIDPAFLYISDPTGTVAPEKCLFGAMLNIAAVLCAIIVY 73
 Db 18 ALIFEVQQFFV-YTIAVLTKHDDPFLPFYVLSAADRPOSQFAIGANISSLLALVVFV 75
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Accession: B69312
 A;Reference: A69250; MUID:3804943; PMID:389475
 A;Molecule type: DNA
 A;Residues: 1-32 <XLE>
 A;Cross-references: UNIPROT:029749; UNIPARC:UPI00000570AA; GB:AE0000782; NIDC
 Query Match 7.4%; Score 103; DB 2; Length 332;
 Best Local Similarity 17.0%; Pred. No. 0.18;
 Matches 45; Conservative 47; Mismatches 112; Indels 60; Gaps 8;
 Qy 2 WFFQQLSFL-----PSALVIWTSAAFISYVITAVTLH----1 36
 Db 65 WWTETGRMLLIEFFRSLLKNTRYLDRVSQKDARLWLFCILFHSSLVLRISRFFL 124
 Qy 37 DPALPYTISDTGTVAPACLGAMLNIAAVLCAIIVYKVQVHALSPPEENVIKLNKAGL 96
 Db 125 DPVPSPFVTELSEIEAKGVFIPSVMGLAIVAAFLMLRRIELSRRTISLPPSHFAL 184
 Qy 97 VLGILSCLGLSIVANFQKTTLFAA-HVSGAVLTFGMSLIMFVQFTLSYOMQPKTHGKV 155
 Db 185 ILLAATISGNVNMRYFVKADLFAVKEMLMSLMTNIGHAVEVANT-----EPI 233
 Qy 156 FWRILJLIVCGVSALSMLTCSSVHSG-----NFGTDLDEQLKLH--WNPERDGYVL 204
 Db 234 FYVHALASF---LIIAYFPFSKMLHAGGYFESPTRNMPNDNRHVNPMDPADVPLLA 289
 Qy 205 HMITTA-----EWMSMFSSFP 220
 Db 290 KGITVAGRYYVKSKKLWDVTYSMY 313

RESULT 3
 C88456 protein W03A5.2 [imported] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C;Accession: C88456
 C;Anonymous: The C. elegans Sequencing Consortium.
 R;Anonymous: The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological processes, development, behavior, and death. Nature 431, 951-957
 A;Reference number: A75000; MUID:9909613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
 A;Note: published errata appeared in Science 283, 35, 1999; Science 281, 2103, 1999; and
 A;Accession: C88456
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-547 <STO>
 A;Cross-references: UNIPARC:UPI000017A5D2; GB:chr.III; PID:9485161; GSF
 A;Note: weakly similar to gamma-glutamyl carboxylase
 C;Genetics:
 A;Gene: W03A5.2
 A;Map position: 3

Query Match 8.6%; Score 120; DB 2; Length 547;
 Best Local Similarity 21.8%; Pred. No. 0.01; Mismatches 100; Indels 26; Gaps 9;
 Matches 48; Conservative 46; Mismatches 100; Indels 26; Gaps 9;

Qy 51 PEKCLFGAMLNIAAVLCAIIVYKVQVHALSPPEEN--VIIKLNKAGLVGILSCLGLS 107
 Db 14 PAKNAYTMINHILLLSVWMLKRELSRFLFIKGSRVNLPGLAALTSYQ 73

Qy 108 VSALSMITSSVLLHSGNFTDLEOKLNHNP-EKGYVHMITTAEWSMSFSFGFLITY 226
 Db 128 --SLAFVVS-----LGAAMIQ-ANTVDPDSQYL-AIDAYEWCYCFAFCVFLTD 175

Qy 227 IRDFQKISLR-VEANLHGHLTYDT--APCPINNERTRL 262
 Db 176 AYERFMMFKPKLIIIRGCTGYNERVESCDVSEDEDNTL 215

Qy 1 MWFFQQQLSFLPSALVIWTSAAFISYVITAVTLHIDPALPVISDGTVAPEKCLFGAML 60
 Db 805 MFW-----AIWSLDLITFSYLDSTSITLWHYNG----SEAGAVVRSVTMSSL 847

RESULT 4
 E69312 nitrate reductase gamma subunit homolog - Archaeoglobus fulgidus

Db	848 PAAIAAMVAWALIRNLPGGLEVLVLSRINMRQASAYAATTILNVIYIAGANTVFGSLGV	907	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-495 A;Cross-references: UNIPARC:UPI000008E589 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Qy	103 -----CLGLSIVANPQKTTLFAAHSGAVLT-----GMGSILYMF 137		
Db	908 SWDKLQWLAALASVGLGLOEFLGNFNSGLKLFERPVRLDVTIGTYSGCTVKIRIR 967		
Qy	138 VQFLISYQNPQPKTHGKQFWIRLLVIVCGVSALSMLTCSSVTHSG-NFGTDLBQKUHN 196		
Db	968 ATTIDDFRKVEVIIPNKA-F-VTERLINV----SISDTTRLVIRLG/VAGSDEK---- 1017		
Qy	197 PDKGYVHLIMITAA-----EWMSFSFFGF-----FLTYIRDFOQKISLRVE 238		
Db	1018 -----VRRVLLQDAMEHPKVMHDPEPAVFFTFGASTLDHELRVYRELDRSHTVD 1069		
RESULT 6			
ET2523	carbon starvation protein A homolog APE2162 [similarity] - Aeropyrum pernix (strain K1)		
C;Species: Aeropyrum pernix			
C;Accession: ET2223	#sequence_revision 20-Aug-1999 #text_change 09-Jul-2004		
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yanazaki, S.; Haikawa, Y.; Jin-no, K.; Takahava, H.; Takanami, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudooh, Y.; Yamazaki, J.; KDNA Res. 6: 83-101, 1999			
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyx			
A;Reference number: A72450; MUID:993:0339; PMID:10382966			
A;Accession: ET2253			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-604 <KAN>			
A;Cross-references: UNIPROT:Q9YQX7; UNIPARC:UPI000005E231; DDBJ:AP000063; NID:95105654;			
A;Experimental source: strain K1			
C;Genetics:			
A;Gene: APE2162			
C;Superfamily: carbon starvation protein			
Query Match			
Best Local Similarity 7.0%	Score 97; DB 2; Length 604;		
Matches 69; Conservative 39; Mismatches 101; Indels 80; Gaps 16;			
Qy	4 FQOGLSFPSAL--VIWVSAAFISFYITAVTLHIDPALPYISDTGVAPEKCLFGAMLN 61		
Db	183 YRMGLGMGSTVTVLVIATTAFYSYNSNGIVIGTDFPSLP-PGEGGWWAYHRWVI-ILG 239		
Qy	62 IAVAVLCIATIVYRKQVHALSPENVILKLNKAGLVGICLSCIGLSTVANFKTTLFAAH 121		
Db	240 LYALLA-PWVY---LLQPRD---YLNAVYLWTG---IGLAAA--AIIQTS 283		
Qy	122 VSGAVLTFGMGSILYMFVQTLISYQMPKIHGKQVFWIRLLVIVCGVSALSMLTCSSVTH 181		
Db	284 LKGPAYT-----SFQNTIAGQPTP-----FWPAIPLIACG---SLSGFHSVLA 325		
Qy	182 SGNFGTDLQKLH-----WN-PB-DKGYY-LHMITTA 210		
Db	326 SGTSKQLASELDALPYGYAMLEGALSGLAVIPISPAWNAPELICGVVIENNMDLA 385		
Qy	211 A-----EWMSFSFFGF-----FLTYIRDFOQKISLRVEANLQLTLYT 249		
Db	386 AVPRYAVGYGYTLAKTFEMFGDTGYSFFTLPASIMLMSMVLTLLDT 434		
RESULT 7			
S43882	NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - garden lettuce mitochondrial		
C;Species: mitochondrial Lactuca sativa (garden lettuce)			
C;Accession: S43882	#sequence_revision 19-Mar-1997 #text_change 09-Jul-2004		
R;Geiss, K.T.; Abbas, G.M.; Makaroff, C.A.			
Mol. Gen. Genet. 243, 97-105, 1994			
A;Title: Intron loss from the NADH dehydrogenase subunit 4 gene of lettuce mitochondrial			
A;Reference number: S43882; MUID:94247363; PMID:819077			
A;Accession: S43882			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-495			
A;Cross-references: UNIPARC:UPI000008E589			
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4			
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;			
Query Match			
Best Local Similarity 24.1%	Score 94; DB 1; Length 495;		
Matches 54; Conservative 34; Mismatches 84; Indels 52; Gaps 11;			
Qy	8 LSFLPSALVINTSAAFISFYITAVTLHIDPALPYISDTGVAPEKCLFGAM-MINI--- 62		

Db	277	LCFTP--FIVTLSAIAIYTSLTTLRQID--LKKITAYSSVAHMNLVTGIMFSLNIOGI	331	A; Reference number: A71630; MUID:99039499; PMID:9823893 A; Accession: F71651 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
Qy	63	-AVLCTATIYRYKO-----VIALSPBENVIRKLNAKGVLV	98	A; Molecule type: DNA A; Residues: 1-429 <AND>
Db	332	GGSILMMSHGLYSSALEFCVGVLDRKTRVLVRYGGLVSTMPNFESTIFFFTLANMSL	391	A; Cross-references: UNIPROT:Q9ZD63; UNIPARC:UPI00000D37BE; GB:AJ235272; NID: A; Experimental source: strain Madrid E C; Genotype: C; Gene: potE; RP483 C; Superfamily: ecotropic retrovirus receptor protein
Qy	99	-GILSCLG--LSIVANFQRTLFLFAAHYSGAVLTFGMSLYMFVQTLISYQMP-----	148	Query Match Score 6.7%; DB 2; Length 429; Best Local Similarity 24.1%; Pred. No. 1..6; Matches 48; Conservative 37; Mismatches 79; Indels 35; Gaps 10;
Db	392	PGTSFFTCBFLVGAFRNSLAVTALGMILGAASWLY-NRVVSGNDLRPDFLYKFS	450	Qy 11 LPSALVIWTAAFISYITAVTLHIDPA-----LPISDTGVAPERCLFGMLN-- 61 217 IPRATIIGTCCVAFYLINSIGLIGIPASELINSKAPY ADAATL-----LFGTWSKV 270
Qy	149	KIHKGQFWIR-LLLVWCGYSALSMU-----SSVLHSGNF	185	Qy 62 --IAAVLCHATI--YVRYKQVHALSPEENVNL-----NKGLVLGILSCLGSLSV 109 271 ITVIASVICITLNAAWLTGQIAAGLAEDGLPFFAKGSNSNNAPTYGIIISCGUITPL 330
Db	451	DNGREVTFPLPLGVWWMGTVPKVLDICMHTSVSNLVORSKF	494	Db 110 ANFOKTTLFAAHVSGAVLTFCMGSLYMFVOTILSYQMPKX-HGKVQFWIRLLVWGV 168 331 LLFTSNNNFKAQIT-QIDFSV-IAFLFVLYLCSAFLKVFSSKENFSYYLF----V 383
RESULT 9				
Db	66506	hypothetical protein T12C22.2 [imported] - Arabidopsis thaliana		R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
C; Species: Arabidopsis thaliana (mouse-ear cress)				
C; Accession: D96516				
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_Change 09-Jul-2004				
R; Theologis, A.; Ecker, J.R.; Palme, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizat, L.				
Nature Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzali, R.; Russo, M.; Rooney, T.; Rowley, D.; Sakano, H.				
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.				
A; Title: Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis</i> .				
A; Reference number: A86141; MUID:21016719; PMID:11130712				
A; Accession: D96516				
A; Status: preliminary				
A; Molecule type: DNA				
A; Residues: 1-379 <STO>				
A; Cross-references: UNIPROT:Q9LDP6; UNIPARC:UPI000000BF00; GB:AE005173; NID:98655985; PI				
C; GenBank: T12C22.2				
A; Map position: 1				
C; Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70				
Query Match Score 6.7%; DB 2; Length 379;				
Best Local Similarity 21.8%; Pred. No. 1..4;				
Matches 47; Conservative 53; Mismatches 95; Indels 21; Gaps 9;				
Qy 10 FLPSALVIWTAAFISYITAVTLHIDPALPYISDTGTVAPEKCFG-AMINTAA---				
Db 90 YIP-LLIUPSSAVSESSSCSLKYI--VLIYVLLGVIAGDNMLYVSGLLYLASYS				
145 65 VLCTATIYRYKQVHALSPEENVTLKINKAGLVIGILSCLGLSIVANFQKTLFAAHVSG 124				
Db 146 LICATOLAFNAVEFYFINAQKFPTALINSLVVSALIAANDDAPPSGSRSKYVG 205				
Qy 125 AVLTFGMSGLYMFVQTLISYQMPKIKHGKQVFMIRLLVWCGVSALSMLTCSVLSHGN				
Db 206 FVCTLAAASLYSLISLQMSQSPE-KILKRETFSVLQENQIYTSVLA---TCVSVI--GL 258				
Qy 185 FGTDLQKHWNPE--DKG--TVLHMFTAWSM				
Db 259 FASGEWRTLHGENGYHKQASSTVLTWTAIWQV				
294				
RESULT 10				
F71651				
C; Species: Putrescine-ornithine antiporter (potE) RP483 - Rickettsia prowazekii				
C; Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 05-Oct-2004				
R; Accession: S7611; S.G.E.; Zomordipour, A.; Andersson, J.O.; Sicheritz-Pontem, T.; Alsmark, U.				
Nature 396, 133-140, 1998				
A; Title: The genome sequence of <i>Rickettsia prowazekii</i> and the origin of mitochondria.				

submitted to the EMBL Data Library, December 1995

A; Reference number: 219897

A; Accession: T24487

A; Status: preliminary, translated from GB/EMBL/DDJB

A; Molecule type: DNA

A; Residues: 1-373 <WIL>

A; Cross-references: UNIPROT:Q22188; UNIPARC:UPI0001641C3; EMBL:Z68219; PIDN:CAA92481.1;

A; Experimental source: clone TOSA1

C; Genetics:

A; Gene: CESD:T05A1.1

A; Map position: 4

A; Introns: 48/2; 106/3; 219/2; 254/1; 280/1; 309/1; 327/2

Query Match 6.6%; Score 91.5; DB 2; Length 373;

Best Local Similarity 23.0%; Pred. No. 2;

Mismatches 34; Indels 51; Gaps 11;

Matches 50; Conservative 34;

Query 69 ATIYVRYKQVHALSPEENVIKLINKAGVIGLISCLGLISIVANFQKTLEAH-----121

Db 46 AVLYLTMH-RQLQTQVNLIFILNLCASNVLMCLTSPLPTFTINVKQWFSSPVCKLPL 104

Query 122 VSGA---VLTFGMSLVMFVQTTLSYQNPQPKHGKVFWIRLLVWCGVSALSMLTCSS 178

Db 105 VQGASIFSTPSLSAIALDRYNLVRPKQKLSSRSAMMIAL--IW---VISVVVVCMP 158

Query 179 VLHSGNFRGTDLE-QKL-----HWNPED--KGTVLHMITTAEWSMSFSFFGFLLT 225

Db 159 -----YGYMDVEKLNGLICGTYCSEHIMPLAEYRKGYTFVLIT---QFLFPFATMFC 208

Query 226 YIRDFOKISLRVEANLHSITLYDTAPCDINNETRLL 262

Db 209 YYNTFSRURQRVETKLKL-----SERSQLL 234

Search completed: August 28, 2006, 17:37:16

Job time : 59 secs

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OM protein - protein search, using SW model

Run on: August 28, 2006, 17:31:24 ; Search time 300 Seconds
 (without alignments)
 820,180 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

Sequence: 1 MWWFQQGLSFLPSALVITW.....YDTPAPCPINNERTRLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 1500 summaries

Database : UniProt 7.2:
 1: uniprot_sprot:
 2: uniprot_trembl:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1392	100.0	266	2	Q6DX65_HUMAN	Q6ux65_homo_sapien	
2	1383	99.4	266	2	Q41WF6_HUMAN	Q4vwf6_homo_sapien	
3	1295	93.0	266	2	Q3ZG48_BOVIN	Q3zc48_bos_taurus	
4	1236	89.4	267	2	Q9CR48_MOUSE	Q9cr48_m_10_days_e	
5	1235	88.8	267	2	Q5BK09_RAT	Q5bk09_ratetus_norv	
6	1235	88.7	267	2	Q9D520_MOUSE	Q9d520_mus_musculus	
7	805	57.9	180	2	Q9DB35_MOUSE	Q9db35_mus_musculus	
8	764.5	54.9	272	2	Q6IQ10_BRARE	Q6iq10_brachydanio	
9	725	52.1	136	2	Q8NBQ4_HUMAN	Q8nbq4_homo_sapien	
10	492.5	35.4	238	2	Q8NE82_HUMAN	Q8ne82_homo_sapien	
11	479.5	34.4	238	2	Q9DC58_MOUSE	Q9dc58_mus_musculus	
12	477.5	34.3	240	2	Q5XK0L_BRARE	Q5xj10_brachydanio	
13	476.5	34.2	240	2	Q5REJ7_BRARE	Q5rgj7_brachydanio	
14	473.5	34.0	239	2	Q5EAK8_XENTR	Q5eak8_xenopus_tro	
15	471.5	33.9	287	2	Q6NRS6_XENLA	Q6nrs6_xenopus_lae	
16	470.5	31.6	238	2	Q8QGB2_ONCIMA	Q8qgb2_oncorhynchus	
17	388.5	27.9	237	2	Q7O651_ANOGA	Q7qe61_anophelis_g	
18	361.5	26.0	246	2	Q5XK0L_BRARE	Q5xj10_brachydanio	
19	338.5	23.9	267	2	Q5DAX3_SCJHA	Q5dax3_schistosoma	
20	318.5	22.9	252	2	Q86F93_SCJHA	Q86f93_schistosoma	
21	289.5	20.8	232	2	Q32PK2_BRARE	Q32pk2_brachydanio	
22	288	20.7	271	2	Q93319_XENLA	Q93319_caenorhabdi	
23	277	19.9	73	2	Q4T6B8_TETNG	Q4t6b8_tetraodon_n	
24	267.5	19.2	231	2	Q4V7T3_XENLA	Q4vt3_xenopus_lae	
25	260	18.8	238	2	Q8R218_MOUSE	Q8r218_mus_musculus	
26	260	18.7	293	2	Q6LP61_CAEVR	Q6lp61_caenorhabdi	
27	258.5	18.6	230	2	Q4V7T7_XENLA	Q4vt7_xenopus_lae	
28	251.5	18.1	181	2	Q5XHF5_DROYA	Q5xhf5_drosophila	
29	231	18.0	132	2	Q9NTN1_HUMAN	Q9ntn1_homo_sapien	
30	248	17.8	257	2	Q5DGL6_SCJHA	Q5dgl6_schistosoma	
31	247	17.7	132	2	Q5EAR39_BOVIN	Q5ear39_bos_taurus	

32	240	17.2	132	2	Q78J26_MOUSE	Q78j26_mus_musculus	
33	203	14.6	249	2	Q8C8S3_MOUSE	Q8c8s3_mus_musculus	
34	201.5	14.5	271	2	Q6GP14_XENLA	Q6gp14_xenopus_lae	
35	191.5	13.8	257	2	Q6IQJ3_BRACHYDANIO	Q6iqj3_brachydanio	
36	188.5	13.5	308	2	Q4SA40_TETNG	Q4sa40_tetraodon_n	
37	185.5	13.3	219	2	Q6P6P1_MOUSE	Q6p6p1_mus_musculus	
38	183.5	13.2	294	2	Q7SXK4_BRACHYDANIO	Q7sxk4_brachydanio	
39	174.5	12.5	243	2	Q559G4_DICIDI	Q559g4_dicyostegeli	
40	172.5	12.4	243	2	Q86IK0_DICIDI	Q86ik0_dicyostegeli	
41	161.5	11.6	123	2	Q8C9L9_MOUSE	Q8c9l9_mus_musculus	
42	160.5	11.5	271	2	Q86TG1_HUMAN	Q86tg1_homo_sapien	
43	157.5	11.3	271	2	Q9QZB9_RAT	Q9qzb9_rat	
44	153.5	11.0	760	2	Q4SKZ5_TETNG	Q4skz5_tetraodon_n	
45	151.5	10.9	271	2	Q91WN2_MOUSE	Q91wn2_mus_musculus	
46	150.5	10.8	243	2	Q86K17_DICIDI	Q86k17_dicyostegeli	
47	147.5	10.6	251	2	Q556P1_DICIDI	Q556p1_dicyostegeli	
48	133.5	9.6	233	2	Q4T6B7_TETNG	Q4t6b7_tetraodon_n	
49	125.5	9.0	147	2	Q3TL7B_MOUSE	Q3tl7b_mus_musculus	
50	121.5	8.7	241	2	Q23135_CAEVL	Q23135_caevl	
51	120.5	8.7	207	2	Q550K4_DICIDI	Q550k4_dicyostegeli	
52	119.5	8.6	273	2	Q628C5_CAEVR	Q628c5_caevr	
53	117.5	8.4	246	2	Q61US8_CAEVR	Q61us8_caevr	
54	113	8.1	362	2	Q3S118_RALSTONIA	Q3s118_ralstonia_m	
55	112.5	8.1	252	2	Q9U3J7_CAEVL	Q9u3j7_caevr	
56	1112	8.0	307	2	Q474C6_RALEJ	Q474c6_ralstonia_e	
57	110.5	7.9	193	2	Q5C7G1_SCHJHA	Q5c7g1_schistosoma	
58	107.5	7.7	435	2	Q7QJU9_ANOGA	Q7qju9_anophelis_g	
59	106.5	7.7	140	2	Q8K117_MOUSE	Q8k117_mus_musculus	
60	105.5	7.6	207	2	Q54KE7_DICIDI	Q54ke7_dicyostegeli	
61	105.5	7.6	881	2	Q5HAJ2_EHRICHIA	Q5haj2_ehrlichia_r	
62	104.5	7.5	217	2	Q5NE86_FRATT	Q5ne86_frattisella	
63	104.5	7.5	229	2	Q2WMT5_CLOSTRIDIUM	Q2wmt5_clostridium	
64	103	7.4	299	2	Q6CD55_YARROWIA	Q6cd55_yarrowia_li	
65	103	7.4	332	1	HMB6_ARCFU	HMB6_arachaeoglob	
66	103	7.4	643	2	Q55R5B_CRYNE	Q55rb8_cryptococcus	
67	103	7.4	643	2	Q5KG8_L_CRYNE	Q5kg8_l_cryptococcus	
68	101.5	7.3	255	2	Q9VP7_DROME	Q9vp7_drosophila	
69	101.5	7.3	332	2	Q650W2_ORYSA	Q650w2_oryza_sativa	
70	101.5	7.3	881	2	Q5FG25_BHRRG	Q5fg25_bhrrg	
71	101	7.3	218	2	QBN2R6_HUMAN	Qbn2r6_homo_sapien	
72	101	7.3	293	1	Q65RP9_MANSM	Q65rp9_mannehima	
73	101	7.3	495	1	N4M_ARATH	N4m_arath	
74	101	7.3	539	2	Q46JE2_SHEON	Q46je2_sheonaria	
75	100	7.2	347	2	Q46F94_MEHTBA	Q46f94_mehtba	
76	99	7.1	305	2	Q3YR32_EHRCW	Q3yr32_ehrcw	
77	98.5	7.1	456	2	Q5D428_ERWCWT	Q5d428_erwcwt	
78	98.5	7.1	71	2	Q5PF14_SALPA	Q5pf14_salpa	
79	98.5	7.1	1120	2	Q82RA5_SALTY	Q82ra5_salty	
80	98.5	7.1	1120	2	Q82BT6_SALTC	Q82bt6_salticidae	
81	98.5	7.1	1140	2	Q57SB5_SALCH	Q57sb5_salchidae	
82	98	7.0	495	2	Q6YSNO_BRANA	Q6ysno brassica_napus	
83	98	7.0	495	2	Q8m8A9_BETVU	Q8m8a9_beta_vulgaris	
84	97.5	7.0	664	2	Q966D8_CAEVR	Q966d8_caenorhabdi	
85	97.5	7.0	746	2	Q9N5Q9_CABEL	Q9n5q9_cabellia	
86	97	7.0	382	2	Q38ZL6_LACSS	Q38zl6_lacistema	
87	97	7.0	390	2	Q8XQMO_RALSO	Q8xqmo_ralstonia	
88	97	7.0	604	2	Q9YKX7_AERPE	Q9ykx7_aeropyrum_p	
89	96.5	6.9	608	2	Q4HK42_GIBZEE	Q4hk42_gibzee	
90	96	6.9	639	2	Q38YX3_LACSS	Q38yx3_lacistema	
91	96	6.9	395	2	Q9BFV0_SHEON	Q9bfv0_sheonaria	
92	96	6.9	460	2	Q3A8B8_PELCASS	Q3a8b8_pelcassia	
93	96	6.9	495	2	Q37544_LACSTU	Q37544_lactucina	
94	96	6.9	535	2	Q22BK9_9GANMM	Q22bk9_9ganmm	
95	96	6.9	535	2	Q363W2_PSEUDU	Q363w2_pseudomonas	
96	96	6.9	535	2	Q36HJ5_9GANMM	Q36hj5_9ganmm	
97	96	6.9	572	2	Q4BVX0_CROWNT	Q4bvx0_crowntia	
98	96	6.9	615	2	Q7S1C6_NEUCPL	Q7s1c6_neucplis	
99	95.5	6.9	628	2	Q5WSU3_LEGPL	Q5wsu3_legume	
100	95.5	6.9	284	2	Q4ZWZL_PSEUDU	Q4zwzl_pseudomonas	
101	95.5	6.9	291	2	Q9ZFP3_ENTFC	Q9zfp3_entrococcus	
102	95.5	6.9	309	2	Q6NRD6_XENLA	Q6nrd6_xenopus_lae	
103	95.5	6.9	388	2	Q4PDK8_USTMNA	Q4pdk8_ustimana	
104	95.5	6.9	486	2	Q8FQF5_COREP	Q8fqf5_corep	

105	95	6.8	440	2	Q4WU03 ASPFU	aspergillus	Q9lnf0 arabidopsis
106	95	6.8	699	2	Q38Vm9 LACSS	lactobacill	Q2zy24 streptococc
107	95	6.8	702	2	Q3Sc10 -MAGNS		Q73JH5 treponema
108	95	6.8	1120	2	Q32D1 SHIBS	shigella a	Q54J51 dictyosteli
109	94.5	6.8	229	2	Q4R14 TETNG	shigella bo	Q8nub1 corynebacte
110	94.5	6.8	268	2	Q5X17 LGPA	terraod n	Q8ff63 escherichia
111	94.5	6.8	463	2	Q41C9 9BACI	legionella	Q9kn89 vibrio chol
112	94.5	6.8	469	2	Q7UF66 RHOBIA	exiguobacte	Q4b023 terraodon n
113	94.5	6.8	724	2	Q6FEU10 -CANGA	rhodopirell	P48915 chondrus cr
114	94	6.8	266	2	Q4FWG7 LEIMA	candida gla	Q4Op99 desulfuromo
115	94	6.8	283	2	Q8BMV8 PSEPK	leishmania	Q5aeg5 candida alb
116	94	6.8	452	2	Q5T19 LACAC	pseudomonas	Q886v4 pseudomonas
117	94	6.8	495	1	NUAM_WHEAT	lactobacill	Q8GJF7 bialloviibri
118	94	6.8	542	2	Q30BS5 9GAMM	pseudomonas	Q877D2 pyrococcum
119	94	6.8	543	2	Q3NTZ4 -SHFR	shewanella	Q5a3n6 candida alb
120	94	6.8	820	2	Q6IKL4 CAEGR	shewanella	Q5a3r1 pasteurella
121	94	6.8	1120	2	Q8F90 BCOL6	caenorhabdi	P44855 haemophilus
122	93.5	6.7	303	2	Q2V417 ARATH	escherichia	Q6mkw0 bdelovibri
123	93.5	6.7	367	2	Q3ETM0 ARATH	arabidopsis	Q886v4 pseudomonas
124	93.5	6.7	379	2	Q9lpF6 ARATH	pseudomonas	Q30pv3 thiomicrosp
125	93.5	6.7	429	2	Q9zd63 RICPR	rickettsia	Q9c114 pasteurella
126	93.5	6.7	440	2	Q4Qmf2 -HAEL8	haemophilus	Q4Op99 haemophilus
127	93.5	6.7	680	2	Q3GbW9 FIRM	syntrophomo	Q65QD7 manheimia
128	93.5	6.7	1624	2	Q41335 G1BZE	giberella	Q929t2 listeria in
129	93	6.7	576	2	Q52SX8 -LEGPH	legionella	Q41zv5 desulfuroba
130	93	6.7	688	2	Q43CS1 RHOPHA	rhodopseudo	Q57L25 salmoneilla
131	93	6.7	797	2	Q455B5 CAEEL	caenorhabdi	Q4v1g2 bacillus ce
132	93	6.7	1120	1	KEFA_ECOLI	pseudomonas	Q88t41 lactobacill
133	93	6.7	1120	2	Q3245 SHIDS	shigella dy	Q65QD7 manheimia
134	93	6.7	1120	2	Q324T4 SWISS	shigella so	Q929t2 listeria in
135	93	6.7	1120	2	Q2NbM2 -ECOLI	Q2mbw	Q41zv5 desulfuroba
136	93	6.7	1120	2	Q8xD54 ECOP57	escherichia	Q52yy3 legionella
137	93	6.7	1120	2	Q838E8 SHIGELLA	shigella fl	Q53i37 bradyrhizob
138	93	6.7	1264	2	Q6BT03 SHIFL	shigella fl	Q3dacf9 streptococc
139	92.5	6.6	251	2	Q970A1 SULTO	debaryomyce	Q3dhf4 streptococc
140	92.5	6.6	473	2	Q8ZNC5 SALTY	Q970a1 sulfolobus	Q3dtm1 streptococc
141	92.5	6.6	473	2	Q8Z506 -SALTI	Q8znc5 salmonella	Q3K170 streptococc
142	92.5	6.6	479	2	Q6S6M5 9BACT	Q8z506 salmonella	Q8dzr0 streptococc
143	92.5	6.6	538	2	Q33W09 9GAMM	Q6S6M5 uncultured	Q8ezh7 streptococc
144	92.5	6.6	634	2	Q5KSp7 -9BCHI	Q33W09 shewanelle	Q22089 canenorhabdi
145	92.5	6.6	977	2	Q6CK54 KLUHM	Q5ksp7 astropsecten	Q3dhf4 streptococc
146	92.5	6.6	1117	2	Q4KUf2 PBFB5	kluyveromyc	Q3npv4 shefrr
147	92	6.6	399	2	Q3P0W7 -9GAMM	Q4kjf2 pseudomonas	Q8bv59 mus musculu
148	92	6.6	434	2	Q7Vn68 HABDU	Q3p0w7 shewanelle	Q8Dzr0 streas5
149	92	6.6	449	2	Q2jYC6 RILET	Q7vn68 haemophilus	Q8212m6 bacillus ce
150	92	6.6	454	2	Q512J7 -ENTHI	Q2jyc6 rhizobium e	Q27yr56 rhodopseudo
151	92	6.6	594	2	Q5V2N6 HALIMA	Q512J7 entamoeba h	Q37rt8 giardinia lam
152	91.5	6.6	568	2	Q52BL1 LEGPH	Q5v2n6 halarcin	Q3npv4 shefrr
153	91.5	6.6	279	2	Q3V299 -ENTFC	Q52rl1 legionella	Q8bv59 mouse
154	91.5	6.6	387	2	Q21188 -CABEL	Q3y299 enterococcu	Q8zj45 yersinia pe
155	91.5	6.6	430	2	Q81014 CABEL	Q21188 caenorhabdi	Q7tmp35 vibrio vuln
156	91.5	6.6	444	2	Q67en8 -CALSI	Q81014 caenorhabdi	Q22189 q98h9 human
157	91.5	6.6	447	2	Q5q224 -IDIL0	Q67en8 callinectes	Q22189 q98h9 human
158	91.5	6.6	447	2	Q5UC11 BETVU	Q5q224 idiomarin	Q7vuy3 bordetella
159	91.5	6.6	495	2	Q9mf62 BETVU	Q5u6c1 beta vulgar	Q7wb6d bordetella
160	91.5	6.6	530	2	Q8W48 -LACPL	Q9mf62 betavulgar	Q9ufa2 homo sapien
161	91.5	6.6	712	1	POT1_ARATH	Q8W48 laccolictes	Q9h698 yersinia pe
162	91.5	6.6	712	2	0567D6 ARATH	Q96y66 arabidopsis	Q96f81 homo sapien
163	91	6.5	732	2	Q4wc47 ASPFU	Q59224 idiomarin	Q96f81 homo sapien
164	91.5	6.6	793	2	Q3SiJ3 TRIDA	Q9bjy8 condaminea	Q96f81 homo sapien
165	91.5	6.6	1085	2	Q7VQ99 BLQFL	Q9bjy8 thioacetill	Q96f81 homo sapien
166	91.5	6.6	1117	2	Q3Kj67 -PEBPF	Q7VQ99 blochmannia	Q5x183 legionella
167	91.5	6.6	1221	2	Q4Q682 LEIMA	Q3Kj67 pseudomonas	Q5xxu0 cryrococcu
168	91	6.5	267	2	Q6H1W4 BACHK	Q4ixm4 azotobacter	Q5km52 cryrococcu
169	91	6.5	340	2	Q4WC47 ASPFU	Q4bvq2 crocosphaer	Q9v210 pyrococcu
170	91	6.5	372	2	Q5NU05 ZINMO	Q4bvq2 crocosphaer	Q2mv24 dunaliciella
171	91	6.5	552	2	Q8NKB5 SPAW	Q4bvq2 crocosphaer	Q9sbv7 vanilia cape
172	91	6.5	552	2	Q7NNJ3 BORBR	Q4bvq2 crocosphaer	Q250co salinibacte
173	91	6.5	554	2	Q37E19 RIOPA	Q7NNJ3 bordetella	Q8mbv0 vahnia cape
174	90.5	6.5	331	2	Q6C1J8 KJUTLA	Q37E19 rhodopseudo	Q9tjp3 similia viri
175	90.5	6.5	337	2	Q4NLG6 9MICC	Q6C1J8 kluveromyce	Q9tjp3 similia viri
176	90.5	6.5	443	2	Q5JH08 PIRKO	Q4nlg6 arthrobacte	Q5cz47 caenorhabdobi
177	90.5	6.5	579	2	Q3DLR9 STRAG	Q5jho8 pyrococcus	Q21453 caenorhabdobi

251	88.5	833	2	Q7usm4_RHOBA	rhodopirell
252	87.5	1057	2	Q3Pw1_NTHA	nitrobacter
253	88	6.4	2	Q3A731_PELC	pelobacter
254	88	6.3	2	Q4MVA6_BACCE	bacillus ce
255	88	6.3	2	Q632P0_BACZ	bacillus ce
256	88	6.3	2	Q6R7C9_BACHK	bacillus th
257	98	6.3	2	Q81KE4_BACAN	bacillus an
258	88	6.3	2	Q4SP91_TETPH	tetraodon n
259	88	6.3	2	Q2RKU5_MOOTH	moorella th
260	88	6.3	2	Q8A1P0_BACTN	bacteroids
261	88	6.3	2	Q8R792_TBTBN	thermoanaer
262	88	6.3	2	Q4ZTV4_PBEU2	pseudomonas
263	88	6.3	2	Q9TCCL_NEPOL	nephroseimi
264	88	6.3	2	Q469Q3_METBA	methanosaarc
265	88	6.3	2	Q4NGAI_9NICC	anthrobacte
266	88	6.3	2	Q37CM4_RHOPA	rhodopseudo
267	88	6.3	2	Q8PXP0_METMA	methanosaarc
268	88	6.3	2	Q7S317_NEUCA	neurospora
269	88	6.3	2	Q7WMW6_BORBR	bordetella
270	88	6.3	2	Q74F70_GEOBACTER	geobacter s
271	88	6.3	2	Q9TQ91_WARSEWICZI	warzewiczi
272	88	6.3	2	Q37CM4_RHOPA	rhodopseudo
273	88	6.3	2	Q9LG66_ORYSA	uncultured
274	88	6.3	2	Q50TH0_ENTHI	oryza sativ
275	87.5	1165	1	ADCY6_CAFNA	p30804 canis famili
276	87.5	6.3	2	Q9D9W6_MOUSE	q9d2w6 mus musculu
277	87.5	6.3	2	Y117_BORBL	q51144 borrelia bu
278	87.5	6.3	2	Q5NQ68_ZINMO	05nq68 zymononas m
279	87.5	6.3	2	Q48LW2_PEE14	q48lw2 pseudomonas
280	87.5	6.3	2	Q50TH0_ENTHI	q50th0 entanothi h
281	87.5	6.3	2	Q3G5Z3_CHLVI	q39gz3 prosthococh
282	87.5	6.3	2	MRAY_LEGPH	q5zsaz2 legionella
283	87.5	6.3	2	Q6KIR7_MYCMO	q5khr7 mycoplasma.
284	87.5	6.3	2	Q3FU92_9BURK	q3fu92 rhodoflex
285	87.5	6.3	2	Q4U811_RCFE	q4u811 rickettsia
286	87.5	6.3	2	Q6BWP9_RACTY	q6bpw9 rickettsia
287	87.5	6.3	2	Q9KRP3_VIBCH	q9krp3 vibrio chol
288	87.5	6.3	2	Q5ERCL_MOUSE	q9qz18 mus musculu
289	87.5	6.3	2	Q64ZW5_9ANNB	q64zw5 clymenella
290	87.5	6.3	2	Q3UZ93_MOUSE	03uz93 m 8 days em
291	87.5	6.3	2	Q7TNKO_RAT	q7tnko rattus norv
292	87.5	6.3	2	Q6BQ78_DBBA	q6bq78 debaryomye
293	87.5	6.3	2	Q5PN23_SALPA	q5pn23 salmonella
294	87.5	6.3	2	YPIGB_BACSU	q54723 bacillus su
295	87.5	6.3	2	Q5XG4_LGPNA	q58g4 legionella
296	87.5	6.3	2	Q8ENR7_OCBIEH	q8enr7 oceanobacter
297	87.5	6.3	2	Q18061_CAEEL	q18061 caenorhabdi
298	87.5	6.3	2	Q82AX5_CHLCV	q84x5 chlamydophi
299	87.5	6.3	2	Q73WX6_MCPNA	q73wx6 mycobacteri
300	87	6.3	2	Q7FTQ2_HADCU	q9jq2 rustici spie
301	87.5	6.3	2	Q7QBT7_ANOGA	q7qbt7 anophiles g
302	87.5	6.3	2	Q4JSL6_CORJK	q4jsl6 corynebacte
303	87.5	6.3	2	Q6Q117_RAT	q6q117 rattus norv
304	87	6.2	2	Q4SFA4_TETPH	q4sfa4 tetrabacter
305	87	6.2	2	Q4VOX1_BACZZ	q4vox1 tetradon n
306	87	6.2	2	Q7VLY2_HADCU	q7vly2 hemophilus
307	87	6.2	2	Q45BS9_HABDU	q5bs9 burholderi
308	87	6.2	2	Q63LJ0_BURPS	q63lj0 burholderi
309	87	6.2	2	Q4J7T0_STLAC	q4j7t0 sulfobolus
310	87	6.2	2	Q6FFP1_ACTAD	q6ffp1 actinobact
311	87	6.2	2	Q3H552_NOCARDIA	q1h552 nocardioide
312	87	6.2	2	Q8X5A2_ECHERICHIA	q8x5a2 escherichia
313	87	6.2	2	Q62BS8_BURPS	q62bs8 burholderi
314	87	6.2	2	Q61LJ0_BURPS	q61lj0 burholderi
315	87	6.2	2	Q2YRS5_NENTR	q2yrs5 kluverra as
316	87	6.2	2	EKOQ_RHIME	q0729 rhizobium m
317	87	6.2	2	Q3EFX5_BURPS	q3efx5 burholderi
318	87	6.2	2	Q3NN43_SHERPA	q3nn43 shewanelle
319	87	6.2	2	Q61B99_CAEEL	q61b99 caenorhabdi
320	87	6.2	2	Q5WU59_LGPNA	q5wu59 legionella
321	87	6.2	2	Q5X2E0_LGPNA	q5x2e0 legionella
322	87	6.2	2	Q5AV43_ENENI	q5ava3 aspergilus
323	87	6.2	2	Q3JF87_BURP1	q3jf87 burholderi
324	87	6.2	2	Q43WI9_SOLUS	q43wi9 solibacter
325	87	6.2	2	Q9I4D1_PSEAB	q9i4d1 pseudomonas
326	87	6.2	2	Q9LEC9_SOLUT	q9lec9 solutum
327	86.5	6.2	2	Q4Q1K2_HAEI8	q4q1k2 haemophilus
328	86.5	6.2	2	Q970T4_SULTO	q970t4 sulfolobus
329	86.5	6.2	2	Q4AMQ7_CHLUL	q4amq7 chlorobium
330	86.5	6.2	2	Q839RL_ENTFA	q839rl enterococcus
331	86.5	6.2	2	Q4691_YCHLUL	q4691 bacillus su
332	86.5	6.2	2	Q4WDR2_ASPPFU	q4wdr2 aspergillus
333	86.5	6.2	2	Q4SY26_TETNG	q4sy26 tetradon n
334	86.5	6.2	2	Q3SD3_TETNG	q3sd3 tetradon n
335	86.5	6.2	2	Q41QU4_FERAC	q41qu4 ferroplasma
336	86.5	6.2	2	Q4UCA2_THEAN	q4uca2 thelleria a
337	86.5	6.2	2	Q5L797_CHLUL	q5l797 chlamydophi
338	86.5	6.2	2	Q6N8M3_RHOPA	q6n8m3 rhodopseudo
339	86.5	6.2	2	Q4KDN8_PSEBF5	q4kdn8 psebf5
340	86.5	6.2	2	Q8ZXCL_TYRAE	q8zxcl tyrae
341	86.5	6.2	2	Q4ERC2_LISMO	q4erc2 lismonia
342	86.5	6.2	2	Q8Y9B6_LISMO	q8y9b6 lismonia
343	86.5	6.2	2	Q7ZV33_BRADY	q7zv33 brachydanio
344	86.5	6.2	2	Q8MKG7_9DIPS	q8mgf7 9dips
345	86.5	6.2	2	Q9TUVB_9GENT	q9tvb 9gent
346	86.5	6.2	2	Q9YCS4_ERPER	q9ycs4 erper
347	86.5	6.2	2	Q4UD84_THEAN	q4ud84 thelleria a
348	86	6.2	2	Q3EZK8_BACTI	q3ezk8 bacteri
349	86	6.2	2	Q4PRM4_GIBBER	q4prm4 gibberella
350	86	6.2	2	Q662P5_BORGIA	q662p5 borgia
351	86	6.2	2	Q8R3W1_MOUSE	q8r3w1 mus musculu
352	86	6.2	2	Q5DBF3_SCHJA	q5dbf3 schizophyllum
353	86	6.2	2	Q3NMX9_SHEWAN	q3nmx9 shewanelle
354	86	6.2	2	Q3GHGP3_CHLUL	q3ghgp3 chlul
355	86	6.2	2	Q4IEC2_JIBAZC	q4iec2 jibazc
356	86	6.2	2	Q2NHA6_STAAZ	q2nha6 staaaz
357	86	6.2	2	Q6GAU7_STAAS	q6gau7 staphylococci
358	86	6.2	2	Q7AG62_STAAN	q7ag62 staphylococci
359	86	6.2	2	Q9VB1_STAAN	q9vb1 staphylococci
360	86	6.2	2	Q9VOC0_PYRAB	q9voc0 pyracobacter
361	86	6.2	2	Q2RBC1_ECOLI	q2rbc1 escherichia
362	86	6.2	2	Q2NAQ9_ECOLI	q2naq9 escherichia
363	86	6.2	2	Q32HY2_SHIDS	q32hy2 shigella dy
364	86	6.2	2	Q7Y8W4_PORTUNUS	q7y8w4 portunus tr
365	86	6.2	2	Q36BY3_GAMM	q36by3 gammaridae
366	86	6.2	2	Q7R5JB_GIALA	q7r5jb giala lam
367	86	6.2	2	Q2JUB9_RHOPA	q2jub9 rhodopseudomonas
368	86	6.2	2	Q2UTV5_ICYAN	q2utv5 cyanobacter
369	86	6.2	2	Q8W9Q3_MESVII	q8w9q3 mesvii
370	86	6.2	2	Q8HTM4_ACHTR	q8htm4 achthromyces
371	86	6.2	2	Q91MM3_ARATH	q91mm3 arabiopsis
372	86	6.2	2	P292949_ARATH	p292949 arabiopsis
373	86	6.2	2	MNPB_STAXY	mnpb staxy
374	86	6.2	2	Q3TRC6_EHRICIA	q3trc6 ehrlichia c
375	86	6.2	2	Q7VGA9_HELHP	q7vga9 helicobacter
376	86	6.2	2	Q8T6H2_DICD1	q8t6h2 dictyostellidae
377	86	6.2	2	Q54EBK2_DICD1	q54ebk2 dictyostellidae
378	86	6.2	2	Q5AVK4_ASPERGILLUS	q5avk4 aspergillus
379	85.5	6.1	2	Q9CY24_MOUSULU	q9cy24 mus musculus
380	85.5	6.1	2	Q9B8L7_MOUSE	q9b8l7 mus musculus
381	85.5	6.1	2	Q6CID8_KLURVERA	q6cid8 kluyveromyces
382	85.5	6.1	2	Q9Cp79_PASMLU	q9cp79 pasmella
383	85.5	6.1	2	Q9K017_NEIMB	q9k017 neisseria m
384	85.5	6.1	2	Q5Fa38_NEIGI	q5fa38 neigella
385	85.5	6.1	2	Q669X3_YERSINIA	q669x3 yersinia ps
386	85.5	6.1	2	Q8ZP11_TERPE	q8zp11 terpene
387	85.5	6.1	2	Q40JK4_EHRCH	q40jk4 ehrlichia c
388	85.5	6.1	2	Q6Tch2_HUMAN	q6tch2 homo sapiens
389	85.5	6.1	2	Q8STD9_LACPIL	q8std9 laccobacillus
390	85.5	6.1	2	Q96K55_HUMAN	q96k55 homo sapiens
391	85.5	6.1	2	Q87nx8_MEETAC	q87nx8 methanotrophicus
392	85.5	6.1	2	Q75PY5_CAVPO	q75py5 cavy porcine
393	85.5	6.1	2	Q89kv1_BRADY	q89kv1 bradyrhizobium
394	85.5	6.1	2	Q2XJ85_PSEPU	q2xj85 pseudomonas
395	85.5	6.1	2	Q3EG9A_ACTSC	q3eg9 actinobacillus
396	85.5	6.1	2	Q5r419_PONPY	q5r419 ponpy

397	453	2	Q5R4G3_PONPY	pongo pygma	Q651L0_ORYSA	oryza sativ
398	470	2	Q4t836_TETNG	terradon n	Q9wz39_THENA	thermotoga
399	482	2	Q3CNC3_ALTAT	pseudoalter	Q18154_CAEEL	cænorhabdi
400	482	2	Q4s4Z6_TETNG	tetradon n	Q9Ln4_ARATH	arabidopsis
401	484	2	Q3Uh23_MOUSE	m 14 days p	Q9f118_ARATH	arabidopsis
402	496	2	Q52m77_CHICK	galus gall	Q952y6_CAEEL	cænorhabdi
403	497	2	Q2BZQ5_9SPHI	salinibacte	Q3374_ARBLI	lrix
404	498	2	Q21287_RECAM	reclinomon	Q5t80_CRYNE	cryptococcus
405	521	2	Q8NB05_HUMAN	homo sapien	Q5kj61_CRYNE	cryptococcus
406	526	2	Q9QX46_BRAR	brachydanio	Q9tf1_Lindenbergi	
407	528	2	Q6A2J4_9LAMI	brandisia h	Q7Uj14_rhodopirell	
408	545	2	Q96J75_HUMAN	homo sapien	Q4q897_leishmania	
409	572	2	Q4xZG8_PLAUCH	plasmodium	Q9ta01_lampetra fl	
410	587	1	TMS33_MOUSE	plasmodium	Q3uars5_MOUSE	mus musculus
411	591	1	TM9S3_HUMAN	protozoa	Q9n04_MOUSE	mus musculus
412	599	2	Q5t857_HUMAN	homo sapien	Q7yf84_neiyamymex	
413	629	2	Q571B0_MOUSE	homo sapien	Q48er6_pseudomonas	
414	682	2	Q81C62_COXB	homo sapien	Q97nvy1_streptococcus	
415	695	2	Q2QN15_ORYSA	homo sapien	Q8u0a2_pyrococcus	
416	703	2	Q9Tlw8_9ASTE	homo sapien	Q3dvgg6_chloroflexu	
417	703	2	Q9tla5_9LAMI	homo sapien	Q2Kx95_bordetella	
418	851	2	Q6F0B9_CANGA	homo sapien	Q2jaa7_frankia sp.	
419	855	2	Q9JY2_ERWCH	homo sapien	Q48er6_pseudomonas	
420	895	2	Q3V7U0_GEOKA	homo sapien	Q97nvy1_streptococcus	
421	895	2	Q96J46_NEUCR	homo sapien	Q83m96_tropheryma	
422	85	2	Q6P7FC6_ACID	homo sapien	Q5yta9_nocardia fa	
423	85	2	Q6Ff26_ACINETOB	homo sapien	Q5zg6_corynebacter	
424	85	2	Q6GCK9_CYPCA	homo sapien	Q74f67_geobacter s	
425	85	2	PSTC1_MYCBO	homo sapien	Q59186_pyrococcus	
426	95	2	PSTC1_MYCTU	homo sapien	Q18j3_entamoeba h	
427	85	2	Q3V7U0_GEOKA	homo sapien	Q83mr3_tropheryma	
428	85	2	Q6Ff26_ACINETOB	homo sapien	Q2x075_shewanella	
429	95	2	Q9N2T7_CABEL	homo sapien	Q2zx65_shewanella	
430	85	2	Q8NR03_CORGL	homo sapien	Q74f67_glycocalyx	
431	85	2	Q2U559_ASPOR	homo sapien	Q4e7g9_wobachia e	
432	85	2	Q7PKH1_ANOGA	homo sapien	Q3q28_entamoeba h	
433	85	2	Q9C8P2_LACLA	homo sapien	Q35q28_bacillus zob	
434	85	2	CAXIB_ORYSA	homo sapien	Q35q30_mactrotis la	
435	85	2	Q96YB7_SULTO	homo sapien	Q411L5_METBU	
436	85	2	Q9N2T7_CABEL	homo sapien	Q9i642_PSEAU	
437	85	2	Q3QR8_GIGAMM	homo sapien	Q48bl8_PSEAU	
438	61	2	Q6By36_DEBHA	homo sapien	Q74f67_glycocalyx	
439	95	2	Q9QXP0_MOUSE	homo sapien	Q46rw6_RALEJ	
440	85	2	Q9B8X9_FALSH	homo sapien	Q511J8_ENTHE	
441	85	2	Q8U79_HALVHO	homo sapien	Q518J7_ENTHE	
442	95	2	Q96YB7_SULTO	homo sapien	Q518J8_ENTHE	
443	85	2	Q4C4C5_CROWT	homo sapien	Q515_vibriofish	
444	85	2	Q3QR8_GIGAMM	homo sapien	Q61z28_cænorhabdi	
445	85	2	Q6By36_DEBHA	homo sapien	Q5Qb30_macrotis la	
446	85	2	Q9QXP0_MOUSE	homo sapien	Q46rw6_RALEJ	
447	85	2	Q9B8X9_FALSH	homo sapien	Q511J8_ENTHE	
448	85	2	Q8U79_HALVHO	homo sapien	Q518J7_ENTHE	
449	85	2	Q96YB7_SULTO	homo sapien	Q515_vibriofish	
450	84.5	6.1	Q4t540_TETNG	homo sapien	Q6C772_yarrawa li	
451	84.5	6.1	Q3t319_ENTFA	homo sapien	Q9z04_purple	
452	84.5	6.1	Q65D18_BACLD	homo sapien	Q9cim1_dshg	
453	84.5	6.1	Q4C0M7_CROWT	homo sapien	P45030_haemophilus	
454	84.5	6.1	Q7Myx3_PHEOL	homo sapien	Q9jvJ1_neisseria m	
455	84.5	6.1	Q3Dmn2_STRAQ	homo sapien	Q9jvJ1_neisseria m	
456	84.5	6.1	Q6ND83_RHOPOA	homo sapien	Q9jvJ1_neisseria m	
457	84.5	6.1	Q2YAJ7_9ARCH	homo sapien	Q9jvJ1_neisseria m	
458	84.5	6.1	Q65FD5_BACLD	homo sapien	Q9jvJ1_neisseria m	
459	84.5	6.1	Q4CON7_CROWT	homo sapien	Q9jvJ1_neisseria m	
460	84.5	6.1	Q7XB13_WHEAT	homo sapien	Q9jvJ1_neisseria m	
461	84.5	6.1	Q5P123_AZOSE	homo sapien	Q9jvJ1_neisseria m	
462	84.5	6.1	Q3DRN2_STRAQ	homo sapien	Q9jvJ1_neisseria m	
463	84.5	6.1	Q7TC08_9INSE	homo sapien	Q9jvJ1_neisseria m	
464	84.5	6.1	SERC1_HUMAN	homo sapien	Q9jvJ1_neisseria m	
465	84.5	6.1	Q52m55_CHICK	homo sapien	Q9jvJ1_neisseria m	
466	84.5	6.1	Q66C42_YERPE	homo sapien	Q9jvJ1_neisseria m	
467	84.5	6.1	Q8Zfw8_YERPE	homo sapien	Q9jvJ1_neisseria m	
468	84.5	6.1	Q35P06_9BAD	homo sapien	Q9jvJ1_neisseria m	
469	84.5	6.1	Q65N12_BACLD	homo sapien	Q9jvJ1_neisseria m	
470	84.5	6.1	Q4t836_TETNG	homo sapien	Q9jvJ1_neisseria m	
471	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
472	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
473	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
474	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
475	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
476	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
477	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
478	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
479	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
480	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
481	84.5	6.1	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
482	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
483	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
484	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
485	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
486	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
487	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
488	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
489	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
490	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
491	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
492	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
493	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
494	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
495	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
496	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
497	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
498	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
499	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
500	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
501	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
502	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
503	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
504	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
505	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
506	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
507	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
508	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
509	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
510	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
511	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
512	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
513	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
514	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
515	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
516	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
517	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
518	84	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
519	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
520	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
521	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
522	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
523	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
524	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
525	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
526	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
527	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
528	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
529	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
530	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
531	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
532	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
533	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
534	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
535	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
536	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
537	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
538	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
539	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
540	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
541	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
542	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
543	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
544	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
545	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
546	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
547	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
548	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
549	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
550	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
551	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
552	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
553	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
554	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
555	83.5	6.0	Q4t540_TETNG	homo sapien	Q9jvJ1_neisseria m	
556	83.5	6.0				

543	83	234	2	Q3UBS2_MOUSE	mus musculu	Q3n287 syntrophobacter	2
544	83	241	1	YLR68_MINTIV	mimivirus	Q75113 asbyna gossypii	2
545	83	6.0	297	OAK95_PBEFS	Oak95 pseudomonas	Q8s184 valeriana j	2
546	83	6.0	305	Q8YWR6_ANASP	Q8ywr6 anabena sp	Q70sp4 limosella m	2
547	83	6.0	318	Q8DNU4_SPRTR6	Q8dn4 streptococcus	Q70sp4_9LAMI	2
548	83	6.0	321	Q85V1_HUMAN	Q8ugf6 homo sapien	Q8sCD0_9ERIC	2
549	83	6.0	321	Q6NFB5_HUMAN	Q8ntb5 homo sapien	Q4t7Y0 tetradon n	2
550	83	6.0	321	Q5SQ19_HUMAN	Q5sq19 homo sapien	Q7ppE3 anopheles g	2
551	83	6.0	324	Q4X186_ASPPU	Q4x186 aspergillus	Q9rCE0_HUMAN	2
552	83	6.0	361	Q3NBQ8_9PROT	Q3nbq8 nitrosomona	Q75250 homo sapien	2
553	83	6.0	387	Q4AAC9_9CHLBU	Q4aac9 chlorobium	Q2st72 mycoplasma	2
554	83	6.0	395	Q2ZQ4N_SHEPU	Q2zqn4 shewanella	Q88hz2 pseudomonas	2
555	83	6.0	395	Q36FT0_9GAMM	Q36fi0 shewanella	Q98jku0 ratulus norv	2
556	83	6.0	397	Q41BP8_9BACI	Q41bp8 exigibacillus	Q87gy0 vibrio para	2
557	83	6.0	427	Q7PQ01_RICSI	Q7pq01 rickettsia	Q9k6y6 bacillus v	2
558	83	6.0	427	Q92HP5_RICCN	Q92hp5 rickettsia	Q9kt03 vibrio chol	2
559	83	6.0	457	Q8ULB5_PTFRU	Q8ulb5 pyrococcus	Q84et2 uncultured	2
560	83	6.0	460	Q9V0Y7_PRTRAB	Q9v0y7 pyrococcus	Q9f166 azovit	2
561	83	6.0	466	Q7VNNG8_HABDU	Q7vnng8 haemophilus	T2R16 RAT	2
562	83	6.0	467	Q6F9P8_ACJAD	Q6f9p8 acinetobacter	Q97m7r1 arath	2
563	83	6.0	474	Q3GPB2_9GAMM	Q3gpb2 psychrobacter	Q97C50 thermoplasma	2
564	83	6.0	496	Q91418_PBBE	Q91418 pseudomonas	Q5m717 xenopus tro	2
565	83	6.0	508	Q2IT23_APDR	Q2it23 aspergillus	Q25590 helicobacter	2
566	83	6.0	511	Q5V404_HALM	Q5v404 haloarcula	Q4iu66 zoogleobacter	2
567	83	6.0	554	Q2YBNL_NITMU	Q2ybnl nitrosospirillum	Q1u676 arabitidopsis	2
568	83	6.0	587	Q8772B_PBSM	Q8772b pseudomonas	Q9m7r1 arachella t	2
569	83	6.0	637	Q15MSU_NSTRU	Q15msu stryngylocoelus	Q9ia38 amborella t	2
570	83	6.0	787	Q3J591_RHOS4	Q3j591 rhodobacter	Q3k5u4 pseudomonas	2
571	83	6.0	802	Q8SZ78_DROME	Q8sz78 drosophila	Q3vgt4 janthaschia	2
572	83	6.0	1139	Q66D6D_YERPS	Q66d6d yersinia ps	Q35z11 shewanella	2
573	83	6.0	1635	Q9C117_MYCGR	Q9c117 mycosphaerae	Q36qy1 shevanella	2
574	83	6.0	2159	Q8RVI01_MAZIE	Q8rv01 zea mays (m)	Q36qy3 rhizobium l	2
575	83	6.0	2159	Q31162_THICR	Q31162 thiomicrosp	Q374m7 nanochaeus	2
576	83	5.9	265	Q3P1G5_9GAMM	Q3p1g5 pseudomonas	Q3rfu1 ralstonia m	2
577	82.5	5.9	271	Q3ORV7_ITIDN	Q3orv7 thiomicrosp	Q93p9 arabitidopsis	2
578	82.5	5.9	281	Q83BV7_CDXBU	Q83bv7 coxiella bu	Q3vtv3 prosthococh	2
579	82.5	5.9	337	Q59QT6_CNAL	Q59qt6 candida alb	P31602 klebsiella p	2
580	82.5	5.9	346	Q8RHO1_METTAC	Q8rho1 methanosaerobicus	Q70xF0 droau	2
581	82.5	5.9	361	Q31162_THICR	Q31162 thiomicrosp	Q74m77 nanoeq	2
582	82.5	5.9	368	Q72K8_THTET2	Q72k8 thermus thet	Q3rfu17 ralstonia	2
583	82.5	5.9	391	1_EPTL_YEAR	1_eptl yeast	Q93p9 arachella t	2
584	82.5	5.9	400	Q7M916_WOLWSU	Q7m916 wolinella s	Q4oleo desulfurobacter	2
585	82.5	5.9	402	Q4HYX9_GIBZEE	Q4hyx9 gibberella	Q8fnv5 corenebacteria	2
586	82.5	5.9	418	Q9HXM9_PSEBM	Q9hxm9 pseudomonas	Q9a8f3 cauveria	2
587	82.5	5.9	432	Q356P0_9RAD	Q356p0 bradyrhizobium	Q74537 schizophyllum	2
588	82.5	5.9	432	Q5P007_SALPA7	Q5p007 salmonella	Q893s6 bifidobacter	2
589	82.5	5.9	437	Q81KCB3_PIAFP	Q81kcb3 plasmoidium	Q09932 cairnsiabacter	2
590	82.5	5.9	439	Q4UJ11_XANC8	Q4uj11 xanthomonas	Q09932 cairnsiabacter	2
591	82.5	5.9	439	Q8PSI4_XANCP	Q8psi4 xanthomonas	Q09932 cairnsiabacter	2
592	82.5	5.9	441	Q3BPG6_XANNC5	Q3bpg6 xanthomonas	Q09932 cairnsiabacter	2
593	82.5	5.9	443	Q2PES4_XANOR	Q2pes4 xanthomonas	Q09932 cairnsiabacter	2
594	82.5	5.9	443	Q6DW4_9CRUS	Q6dw4 triops long	Q09932 cairnsiabacter	2
595	82.5	5.9	451	2_Q82C18_SPRAW	Q82c18 streptomyces	Q09932 cairnsiabacter	2
596	82.5	5.9	452	Q9ZKR4_HLLPJ	Q9zkr4 helicobacter	Q09932 cairnsiabacter	2
603	82.5	5.9	453	Q5RCN8_PONPY	Q5rcn8 pongo pygmaea	Q385s3 trypanosoma	2
598	82.5	5.9	456	2_Q3K677_PSEPF	Q3k677 pseudomonas	Q3Byi7 xanthomonas	2
604	82.5	5.9	462	Q3JD04_NITTOC	Q3jd04 nitrosooccus	Q6F8D1 acinetobacter	2
599	82.5	5.9	462	Q6F011_MESSFL	Q6f011 mesoplasmata	Q8er30 oceanobacter	2
600	82.5	5.9	471	2_Q82J7_ENTIFA	Q82j7 enterococcus	Q04306 homosapien	2
607	82.5	5.9	478	2_Q36A8_9GAMM	Q36a8 shewanella	Q2u3y1 aspergillus	2
608	82.5	5.9	508	2_Q22J4_9GAMM	Q22j4 shewanella	Q8cye9 streptococcus	2
609	82.5	5.9	543	Q8EBL5_SEION	Q8eb05 shewanella	Q97pc0 streptococcus	2
610	82.5	5.9	482	2_Q3K677_PSEPF	Q3k677 pseudomonas	Q39xj4 geobacter m	2
605	82.5	5.9	484	2_Q44H18_CRLSL	Q44h18 chromohalobacter	Q7mkq7 vibrio vulnificus	2
611	82.5	5.9	484	2_Q82J7_ENTIFA	Q82j7 enterococcus	QBD9M9_vibvu	2
612	82.5	5.9	494	1_NU4M_TRIAU	1_nu4m triau	Q4jt26 corynebacter	2
613	82.5	5.9	523	2_Q95055_SIIPN	Q95055 siipn	Q92dg0 listeria in	2
614	82.5	5.9	620	2_Q5KS33_9CHI	Q5ks33 chilobium	UPPP2 clostridium	2
615	82.5	5.9	640	2_Q6MB47_PARWU	Q6mb47 parachlamyd	Q94vh0 varanus gouani	2

689	81.5	325	2	Q973Q6_SULTO	Q9f295_ARATH	Q9f295_arabidopsis	Q21S96_9DELT	411	2	Q2LS96_9DELT	Q6esp5_ORYSA	Q6esp5_sativ	5.8	
690	81.5	351	2	Q5BDJ8_TMEINI	Q5BDJ8_aspergillus	Q5BDJ8_aspergillus	Q6y1k4_RALSTONIA	422	2	Q8Y1K4_RALSTONIA	Q8Y1K4_ralstonia	Q8Y1K4_ralstonia	5.8	
691	81.5	5.9	390	2	QBNC4_HUMAN	QBnc4_homo_sapien	QBnc4_homo_sapien	Q3Zxw4_dehalococco	423	2	Q3Zxw4_dehalococco	Q8x4u5_escherichia	Q8x4u5_escherichia	5.8
692	81.5	5.9	399	2	Q5Ng59_FRMATE	Q5Ng59_francoiseae	Q5Ng59_francoiseae	Q3gmw8_psychrobact	423	2	Q3gmw8_psychrobact	Q5GMM9_9GAMM	Q5GMM9_9GAMM	5.8
693	81.5	5.9	410	2	Q3VWV4_PROTAE	Q3VWV4_prosthecoch	Q3VWV4_prosthecoch	P76037_escherichia	446	2	P76037_escherichia	PUP_ECOLI	PUP_ECOLI	4.46
694	81.5	5.9	422	2	Q229R5_9GAMM	Q229R5_shewanella	Q229R5_shewanella	P461_shewanella	461	1	P461_shewanella	Q31zz2_shewanella	Q31zz2_shewanella	5.8
695	81.5	5.9	423	2	Q360D7_9GAMM	Q360D7_shewanella	Q360D7_shewanella	Q4s3Y1_TERAOON	461	2	Q4s3Y1_TERAOON	Q4s3Y1_TERAOON	Q4s3Y1_TERAOON	5.8
696	81.5	5.9	423	2	Q34FP5_9GAMM	Q34FP5_shewanella	Q34FP5_shewanella	Q87155_vibrio_chol	471	2	Q87155_vibrio_chol	Q3kcc6_PSEPF	Q3kcc6_pseudomonas	5.8
697	81.5	5.9	423	2	Q88CV8_PSEPK	Q88CV8_pseudomonas	Q88CV8_pseudomonas	Q9778_ecoli	479	2	Q9778_ecoli	YRT3_CABEL	YRT3_CABEL	5.8
698	81.5	5.9	425	2	Q4YAK0_PLABE	Q4YAK0_plasmoidium	Q4YAK0_plasmoidium	Q8aa29_bacteroides	479	2	Q8aa29_bacteroides	Q624N5_CAEBR	Q624N5_caebr	5.8
699	81.5	5.9	435	2	Q4VAK0_PLABE	Q4VAK0_plasmoidium	Q4VAK0_plasmoidium	Q7nzq0_chromobacte	483	2	Q7nzq0_chromobacte	Q7pq74_andophelis	Q7pq74_andophelis	4.83
700	81.5	5.9	436	2	Q7VY203_CRYPTV	Q7VY203_cryptospori	Q7VY203_cryptospori	Q7F7Z2_DECAR	485	2	Q7F7Z2_DECAR	Q9fr13_AROGA	Q9fr13_arabidopsis	4.85
701	81.5	5.9	438	2	Q9HuD9_PSEB	Q9HuD9_pseudomonas	Q9HuD9_pseudomonas	Q9fr13_AROGA	485	2	Q9fr13_AROGA	Q8tf71_homo_sapien	Q8tf71_homo_sapien	4.85
702	81.5	5.9	446	2	Q60WD5_CALEBR	Q60WD5_caenorhabdi	Q60WD5_caenorhabdi	Q87155_vibrio_chol	491	2	Q87155_vibrio_chol	Q3kcc6_PSEPF	Q3kcc6_pseudomonas	5.8
703	81.5	5.9	454	2	Q48Kp6_PSEB14	Q48Kp6_pseudomonas	Q48Kp6_pseudomonas	Q9778_ecoli	491	2	Q9778_ecoli	YRT3_CABEL	YRT3_CABEL	5.8
704	81.5	5.9	454	2	Q4ZYB0_PSEB2	Q4ZYB0_pseudomonas	Q4ZYB0_pseudomonas	Q8aa29_bacteroides	491	2	Q8aa29_bacteroides	Q624N5_CAEBR	Q624N5_caebr	5.8
705	81.5	5.9	454	2	Q88Ar2_PSEBM	Q88Ar2_pseudomonas	Q88Ar2_pseudomonas	Q7nzq0_chromobacte	491	2	Q7nzq0_chromobacte	Q7pq74_andophelis	Q7pq74_andophelis	5.8
706	81.5	5.9	454	2	Q4VAK0_PLABE	Q4VAK0_plasmoidium	Q4VAK0_plasmoidium	Q7F7Z2_DECAR	491	2	Q7F7Z2_DECAR	Q9fr13_AROGA	Q9fr13_arabidopsis	5.8
707	81.5	5.9	463	2	Q5D5D2_SECHJA	Q5D5D2_sechiota	Q5D5D2_sechiota	Q91mj8_menangle	491	2	Q91mj8_menangle	Q98v81_dobanthalus	Q98v81_dobanthalus	5.8
708	81.5	5.9	466	2	Q2q338_adoxophyes	Q2q338_adoxophyes	Q2q338_adoxophyes	Q3n807_nitrosonoma	491	2	Q3n807_nitrosonoma	Q3n807_nitrosonoma	Q3n807_nitrosonoma	5.8
709	81.5	5.9	467	2	Q9n1Z2_DROME	Q9n1Z2_drosophilida	Q9n1Z2_drosophilida	Q3n807_nitrosonoma	491	2	Q3n807_nitrosonoma	Q3n807_nitrosonoma	Q3n807_nitrosonoma	5.8
710	81.5	5.9	475	2	Q33RV8_9GAMM	Q33RV8_9GAMM	Q33RV8_9GAMM	Q9778_ecoli	491	2	Q9778_ecoli	YRT3_CABEL	YRT3_CABEL	5.8
711	81.5	5.9	482	2	Q3JEF5_NTLOC	Q3JEF5_nttloc	Q3JEF5_nttloc	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
712	81.5	5.9	485	2	Q18063_CABEL	Q18063_caenorhabdi	Q18063_caenorhabdi	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
713	81.5	5.9	485	2	Q8SYB7_DROME	Q8SYB7_drosophilida	Q8SYB7_drosophilida	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
714	81.5	5.9	485	2	Q9W1Z3_DROME	Q9W1Z3_drosophilida	Q9W1Z3_drosophilida	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
715	81.5	5.9	487	2	Q2Nn79_RSPhN	Q2Nn79_RSPhN	Q2Nn79_RSPhN	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
716	81.5	5.9	510	2	Q345Z3_PSFHE	Q345Z3_psfhe	Q345Z3_psfhe	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
717	81.5	5.9	513	2	Q31ET8_TLICR	Q31ET8_thiomicrosp	Q31ET8_thiomicrosp	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
718	81.5	5.9	517	2	Q4HUN6_GIBZEE	Q4HUN6_gibzee	Q4HUN6_gibzee	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
719	81.5	5.9	524	2	Q4SNu4_TETNG	Q4SNu4_tetng	Q4SNu4_tetng	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
720	81.5	5.9	527	2	Q2NEHK7_RHOS4	Q2NEHK7_rhodobacter	Q2NEHK7_rhodobacter	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
721	81.5	5.9	535	2	Q3J012_RHOS4	Q3J012_rhodobacter	Q3J012_rhodobacter	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
722	81.5	5.9	535	2	Q53111_RHOSE	Q53111_rhoobacter	Q53111_rhoobacter	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
723	81.5	5.9	570	2	Q2SYK8_BURTH	Q2SYK8_burkhideri	Q2SYK8_burkhideri	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
724	81.5	5.9	577	2	Q2U0M4_ASPOR	Q2U0M4_aspergilus	Q2U0M4_aspergilus	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
725	81.5	5.9	615	2	Q2U0X1_ASPOR	Q2U0X1_aspergilus	Q2U0X1_aspergilus	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
726	81.5	5.9	615	2	Q5AY73_ENTHI	Q5AY73_enthi	Q5AY73_enthi	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
727	81.5	5.9	623	2	Q51X5_ENTHI	Q51X5_enthi	Q51X5_enthi	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
728	81.5	5.9	626	2	Q8XUM7_RALSO	Q8XUM7_ralsonia	Q8XUM7_ralsonia	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
729	81.5	5.9	711	2	Q6LH73_PRORR	Q6LH73_photorbacter	Q6LH73_photorbacter	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
730	81.5	5.9	713	2	Q9VWg4_DROME	Q9VWg4_drosophilida	Q9VWg4_drosophilida	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
731	81.5	5.9	724	2	Q8MrA8_DROME	Q8MrA8_drosophilida	Q8MrA8_drosophilida	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
732	81.5	5.9	724	2	Q9Tz26_NEBNT	Q9Tz26_nebnt	Q9Tz26_nebnt	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
733	81.5	5.9	731	2	Q9Tz22_NEBNT	Q9Tz22_nebnt	Q9Tz22_nebnt	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
734	81.5	5.9	732	2	Q9Tz05_RSBE7	Q9Tz05_rhoobacter	Q9Tz05_rhoobacter	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
735	81.5	5.9	734	2	Q98706_RSBE7	Q98706_rhoobacter	Q98706_rhoobacter	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
736	81.5	5.9	741	2	Q71QV9_RSBE7	Q71QV9_rhoobacter	Q71QV9_rhoobacter	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
737	81.5	5.9	745	2	Q5UYP6_HALMA	Q5UYP6_halma	Q5UYP6_halma	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
738	81.5	5.9	855	2	Q6BGA9_PARTE	Q6BGA9_paramecium	Q6BGA9_paramecium	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
739	81.5	5.9	893	2	Q54B6_DICDI	Q54B6_dicyostelli	Q54B6_dicyostelli	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
740	81.5	5.9	1402	2	Q610A1_CBBR	Q610A1_camborhabdi	Q610A1_camborhabdi	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
741	81	5.8	226	2	Q4MVG5_BACCR	Q4MVG5_bacillus	Q4MVG5_bacillus	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
742	81	5.8	226	2	Q81689_BACCR	Q81689_bacillus	Q81689_bacillus	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
743	81	5.8	228	2	Q4L948_STAHU	Q4L948_staphylococcus	Q4L948_staphylococcus	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
744	81	5.8	273	2	Q3GLF0_9GAMM	Q3GLF0_9GAMM	Q3GLF0_9GAMM	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
745	81	5.8	287	2	Q5V2C4_HALMCA	Q5V2C4_haloarcula	Q5V2C4_haloarcula	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
746	81	5.8	293	2	Y417_CHLPR	Y417_chloroflexus	Y417_chloroflexus	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
747	81	5.8	293	2	Q92wds_BETIME	Q92wds_beta	Q92wds_beta	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
748	81	5.8	296	2	Q3SMw5_THLDA	Q3SMw5_thiobacillus	Q3SMw5_thiobacillus	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
749	81	5.8	297	2	Q5NNK8_ZTMMO	Q5NNK8_zymomonas	Q5NNK8_zymomonas	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
750	81	5.8	305	2	Q3M561_ANAVT	Q3M561_anabaena	Q3M561_anabaena	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
751	81	5.8	305	2	Q5J3L3_RAT	Q5J3L3_rat	Q5J3L3_rat	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
752	81	5.8	313	1	RBN_VIBVY	RBN_vibrio	RBN_vibrio	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
753	81	5.8	313	1	Q3NBM5_TRILER	Q3NBM5_trichodesmium	Q3NBM5_trichodesmium	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
754	81	5.8	315	2	Q2WPB2_CLOBLE	Q2WPB2_clostridium	Q2WPB2_clostridium	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
755	81	5.8	347	2	Q3Bul19_XANCL5	Q3Bul19_xanthomonas	Q3Bul19_xanthomonas	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
756	81	5.8	349	2	Q21YV7_YERPE	Q21YV7_yersinia	Q21YV7_yersinia	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
757	81	5.8	375	1	Q597v4_PSEFM	Q597v4_pseudomonas	Q597v4_pseudomonas	Q9778_ecoli	491	2	Q9778_ecoli	Q9778_ecoli	Q9778_ecoli	5.8
758	81	5.8	375	1	Q5NPd7_ZRMNO	Q5NPd7_zymomonas	Q5NPd7_zymomonas	Q9778_ecoli	491	2				

835	5.8	465	2	Q48D16_PSE14	Pseudomonas	Q48d16	2	Q6iT7X8_LEPDU	leptotyphlo
836	80.5	469	2	P93561_SOLTU	solanum tub	P93561	2	Q2Y913_NITROSPOR	nitrososepi
837	80.5	470	2	O9CP81_PASMU	pasturella	O9cp81	2	Q9n5g8_CAEEL	caenorhabdi
838	80.5	472	2	Q44FB5_9BURK	rhizobacter	Q44fb5	2	Q5567U_DICDI	dicyosteli
839	80.5	472	2	Q4LSU9_9BURK	burkholderi	Q4lsu9	2	Q966D7_CABEL	caenorhabdi
840	80.5	473	1	I0LT_BACSU	bacillus su	I0lt	2	Q4WF6T2_ASPPU	aspergillus
841	80.5	475	2	Q6LR41_PHOPR	photobacter	Q6lr41	2	Q94JG1_ORYSA	ryza sativ
842	80.5	478	2	Q3QD94_9GAMM	shewanella	Q3qd94	2	Q5DZV7_ENTHI	entamoeba sp.
843	80.5	518	2	Q2S8B0_9GAMM	haeilla che	Q2s8b0	2	Q6XRA4_9BACT	uncultured
844	80.5	518	2	Q8AX1_BACTN	bacteroides	Q8ax1	2	Q6XJM6_9BRIC	inhambanell
845	80.5	518	2	Q5F6U6_NEIGI	neisseria g	Q5f6u6	2	Q7Wkb7_RALEU	rallsonia e
846	80.5	528	2	Q7DDN3_NEIMB	neisseria m	Q7ddn3	2	Q3HT50_COLDENIA	pr
847	80.5	528	2	Q9JRD7_NEIMA	neisseria m	Q9jrd7	2	Q9TLF3_hemiphrama	anaerbaena va
848	80.5	531	2	Q6KU84_MCMO	mycoplasma	Q6ku84	2	Q19823_ISPHN	allobacillus sp.
849	80.5	534	2	Q2U2A8_ASFOR	aspergillus	Q2u2a8	2	Q73Y59_myco	bacillus ha
850	80.5	536	2	Q6MENS_PARUN	parachlamyd	Q6mens	2	Q9TJU4_CEPOC	cephalanthu
851	80.5	536	2	Q4EUG7_LISMO	listeria mo	Q4eug7	2	Q9LYR7_ARATH	salmoneella
852	80.5	538	2	Q2IM6_9BBLT	anaeromycob	Q2im6	2	Q4WP24_ASPPU	aspergillus
853	80.5	538	2	Q9817_saccharomyc	luculina gra	Q9817	2	Q8ZQN3_SALTY	salmonella
854	80.5	539	2	Q3J5B7_RHO54	rhodobacter	Q3j5b7	2	Q3M4P3_ANAVT	Q3m4p3
855	80.5	539	2	Q21277_RBCAM	reclinomonas	Q21277	2	Q3VGR9_ISPHN	sphegopyxi
856	80.5	560	2	Q89LN8_CLOTE	clostridium	Q89ln8	2	Q9K9X9_BACHD	Q9k9x9
857	80.5	560	2	Q346Z9_RHOPA	rhodopseudo	Q346z9	2	Q8J80_SHEON	shewanella
858	80.5	560	2	Q2IM16_9BBLT	rhodopseud	Q2im16	2	Q57RE9_SALCH	salmonella
859	80.5	560	2	Q98702_NEIBNT	luculina gra	Q98702	2	Q2ZGU0_CALSA	caldicoccus
860	80.5	560	2	Q31JY9_CALCA	calycophyll	Q31jy9	2	Q3BIP1_ACTINOBACI	actinobacil
861	80.5	560	2	Q3S0G1_RALME	ralstonia m	Q3s0g1	2	Q31GZ8_THICR	thiomicrosp
862	80.5	560	2	Q55KN8_CYNNE	cryptococcus	Q55kn8	2	Q6i7H2_CERBA	cercaria ba
863	80.5	560	2	Q5KRAT6_CRYNE	cryptococcu	Q5krat6	2	Q3Pjm4_PAROCOCUS	paracoccus
864	80.5	560	2	Q1193_HUMAN	homo sapien	Q1193	2	Q66d49_YERSINIA	yersinia ps
865	80.5	560	2	Q3MTW3_HUMAN	homo sapien	Q3mtw3	2	Q93KCO_ERWCH	erwinia car
866	80	560	2	Q3VWW7_HUMAN	homo sapien	Q3vww7	2	Q6D4I7_ERWCNT	erwini car
867	80	560	2	Q81K3_BACAN	bacillus an	Q81k3	2	Q7UKZ3_rho	rho
868	80	560	2	Q9HXP7_PEEAE	pseudomonas	Q9hx7	2	Q8DUD9_STRMU	streptococci
869	80	560	2	Q76FP9_STYPL	styelea plic	Q76fp9	2	Q8R25T7_MOUSE	mus musculu
870	80	560	2	Q5J518_PTKO	pyrococcus	Q5j518	2	Q1PJM4_PARDE	paracoccus
871	80	560	2	Q3HAM2_TRLIER	trichodesmi	Q3ham2	2	Q6CTH9_KLULIA	kluyveromy
872	80	560	2	Q4AM06_9BURK	trichodesmi	Q4am06	2	Q66d49_TERPS	terps
873	80	560	2	Q3BQN3_BACTI	bacillus th	Q3bqn3	2	Q5ACY4_LIEIXX	leifsonia x
874	80	560	2	Q81RV2_BACAN	bacillus th	Q81rv2	2	Q5AF82_CANAL	candida alb
875	80	560	2	Q6YCG4_ONYPE	onion yello	Q6ycg4	2	Q5Q54S_9BRAK	bradyrhizob
876	80	560	2	Q4MMH9_BACCE	pyrococcus	Q4mmh9	2	Q5Q54S_9BRAK	bradyrhizob
877	80	560	2	Q6HK25_BACHK	bacillus th	Q6hk25	2	Q5QSP9_ASPOR	aspergillus
878	80	560	2	Q6LRV2_BACAN	bacillus an	Q6lrv2	2	Q88ZD3_LACPL	lactobacillus
879	80	560	2	QSDV0_MMPU	mimosa pud	Qsdv0	2	Q4RKA6_9MICC	Qang89 arthrobacae
880	80	560	2	Q8UJ09_AGRTS	agrobacteri	Q8uj09	2	Q4SJT4_TEING	teing
881	80	560	2	Q3KL76_CHLTIA	chlamidia t	Q3kl76	2	Q5KY68_CHLULIA	jannaschiae
882	80	560	2	Q4MMP0_BACCB	bacillus ce	Q4mp0	2	Q7NV7_CHRVO	chromobacteri
883	80	560	2	Q6AU50_DESPS	desulfotale	Q6au50	2	Q7085_CAEEL	caenorhabdi
884	80	560	2	Q2RGF6_MOOTH	desulfovibrio	Q2rgf6	2	Q3K8Y3_SEPPF	psuedomonas
885	80	560	2	Q2K6L6_RHET	moorella th	Q2k6l6	2	Q83RL6_SHIFLU	vibrion
886	80	560	2	Q8UJ12_RHET	rhizobacter	Q8uj12	2	Q95AK5_9ASTR	Q95ak5 dialypetalu
887	80	560	2	Q2Y635_NTLMU	rhizobacter	Q2y635	2	Q5593T_SYN3	synchocyst
888	80	560	2	Q51723_BACNO	rhizobacter	Q51723	2	Q40EB4_JANOBAC	janaschiae
889	80	560	2	Q4D0S8_TRYCR	bacteroides	Q4d0s8	2	Q2JYF1_RHET	chromobacteri
890	80	560	2	Q4RMW9_TETNG	trypanosoma	Q4rmw9	2	Q3K8Y3_SEPPF	psuedomonas
891	80	560	2	Q3LIN3_PEFHT	trypanosoma	Q3lin3	2	Q7E75B_VIBFL	Q7e75b vibrio fisc
892	80	560	2	Q4MM07_BACCE	trypanosoma	Q4mm07	2	Q94WS19_ASPPU	Q9ws19 aspergillus
893	80	560	2	Q515Q1_CHEFB	trypanosoma	Q515q1	2	Q4KYL0_CAPBU	Q4kyl0 capella bu
894	80	560	2	Q4GEH0_9MYRT	trypanosoma	Q4geh0	2	Q3Z144_SHISS	shigella so
895	80	560	2	Q6L181_METMP	trypanosoma	Q6l181	2	Q31J91_THICR	thiomicrosp
901	80	560	2	Q4KCI5_PBSF5	trypanosoma	Q4kci5	2	Q73Y55_MYCRA	mycobacteri
902	80	560	2	Q9RSB_STAII	trypanosoma	Q9rsb	2	Q5H3W7_XANOR	xanthomonas
903	80	560	2	Q9AC73_SPAN	trypanosoma	Q9ac73	2	Q9UYP1_PYRAB	pyrococcus
904	80	560	2	Q3FD4_9URK	trypanosoma	Q3fd4	2	Q4N1S4_CHEPA	theileria p
905	80	560	2	Q8PCK4_XANAC	trypanosoma	Q8pk4	2	Q93GK1_BACST	bacillus st
906	80	560	2	Q6NF01_CORDI	corynebacte	Q6nf01	2	Q2UCUB8_ASPPU	Q2ucub8 aspergillus
907	80	560	2	Q4MZY0_THEPA	corynebacte	Q4mzy0	2	Q2IL18_9DELT	Q2il18 aeromycob
								Q6my57_ASPPU	Q6my57 aspergillus

981	79.5	5.7	527	2	Q440H4 SOLUS	Q440h4 solibacter	1054	79	5.7	377	2	Q9LXX8 ARATH	Q9lx8 arabidopsis
982	79.5	5.7	535.	2	Q4PKJ2 ORYSA	Q4pkj2 oryza sativ	1055	79	5.7	381	2	Q6fd6 ACIAD	Q6fd6 actinobacter
983	79.5	5.7	539	1	FIIN AGFT7	FIIN agrobacteri	1056	79	5.7	386	2	Q7NC85 GLOV7	Q7nc85 gloeobacter
984	79.5	5.7	542	2	Q2YKC6 BRU2	Q2ykc6 brucella ab	1057	79	5.7	389	2	Q5L913 BACFN	Q5l913 bacteroides
985	79.5	5.7	542	2	Q8TFW3 BRUSU	Q8tfw3 brucella su	1058	79	5.7	389	2	Q64Q99 BACPR	Q64q99 thermotoga
986	79.5	5.7	542	2	Q8TEB8 BRUME	Q8teb8 brucella me	1059	79	5.7	390	2	Q9X158 THEMA	Q9x158 archaeeglob
987	79.5	5.7	542	2	Q577Q8 BRUAB	Q577q8 brucella ab	1060	79	5.7	395	1	HMEB ARCFU	Hmeb arcfu
988	79.5	5.7	544	2	Q64940 9C0RO	Q64940 infectious	1061	79	5.7	400	2	Q3XTS0 9PRTT	Q3xts0 magnetococc
989	79.5	5.7	559	2	Q5L073 9E0KA	Q5l073 Geobacillus	1062	79	5.7	405	2	Q2R4M4 RHORU	Q2r4m4 rhodospiril
990	79.5	5.7	563	2	Q2D9X1 ASPOR	Q2d9x1 gibberella	1063	79	5.7	409	2	Q4TIAN GIBZ6	Q4tian gibberella
991	79.5	5.7	566	2	Q5BKW2 EMENTI	Q5bkw2 aspergillus	1064	79	5.7	409	2	Q6E830 9HEMT	Q6e830 ponina glad
992	79.5	5.7	566	2	Q5EQN7 HYME	Q5eqn7 pessa conde	1065	79	5.7	410	1	P57638 BUCAI	P57638 buchnera ap
993	79.5	5.7	570	2	Q8UF62 ARGTS	Q8uf62 agrobacteri	1066	79	5.7	414	2	Q66R30 YEAST	Q66r30 sacharamyc
994	79.5	5.7	573	2	Q61FV4 BACZZ	Q63fv4 bacillus ce	1067	79	5.7	420	2	Q2RRZ7 9SPRZ7	Q2rrz7 salinibacte
995	79.5	5.7	573	2	Q81V13 BRCAN	Q81v13 bacillus an	1068	79	5.7	423	2	Q3Q6K6 9GAMM	Q3q6k6 shewanella
996	79.5	5.7	588	2	Q41543 GB2Z	Q41543 gibberella	1069	79	5.7	429	2	Q63YGB BURBS	Q63ygb burbs
997	79.5	5.7	593	2	Q6Bm61 DEBHA	Q6bm61 debaryomyce	1070	79	5.7	438	2	Q7ACT1 ECOPL	Q7act1 escherichia
998	79.5	5.7	596	2	Q526S8 ORYSA	Q526s8 oryza sativ	1071	79	5.7	442	2	Q8FGD5 ECOL6	Q8fgd5 escherichia
999	79.5	5.7	598	2	Q7C211 ARGTS	Q7c211 agrobacteri	1072	79	5.7	439	2	Q4WK65 ASPPU	Q4wk65 aspergillus
1000	79.5	5.7	600	2	Q61KCO PHOPR	Q61kco photobacter	1073	79	5.7	443	2	Q4W667 VIBCH	Q4w667 vibrio chol
1001	79.5	5.7	603	2	Q33H54 METHU	Q33h54 methanospir	1074	79	5.7	443	2	Q61LKM2 PHOPCR	Q61lm2 photobacter
1002	79.5	5.7	613	2	Q8CBQ1 MCUSE	Q8cbq1 mus musculu	1075	79	5.7	444	2	Q7VT98 BORPE	Q7vt98 bordetella
1003	79.5	5.7	628	2	Q67ML1 SYMTH	Q67ml1 symbiobacte	1076	79	5.7	444	2	Q7W2C1 BORBR	Q7w2c1 bordetella
1004	79.5	5.7	632	2	Q9A247 BBSPL6	Q9a247 enterobacte	1077	79	5.7	444	2	Q7WR89 RICHTS8	Q7wr89 bordetella
1005	79.5	5.7	635	2	Q2RAF8 ORYSA	Q2raf8 oryza sativ	1078	79	5.7	444	2	Q9KKW1 VIBCH	Q9kkw1 vibrio chol
1006	79.5	5.7	639	2	Q5WCB3 BACSK	Q5wcb3 bacillus cl	1079	79	5.7	446	2	Q6L0U0 PICTAO	Q6lou0 pictorhodobacter
1007	79.5	5.7	643	2	Q2RH29 RHORU	Q2rh29 rhodospirill	1080	79	5.7	447	2	Q6GERO STAAR	Q6gero staphylococ
1008	79.5	5.7	669	2	Q6USQ3 9E0IPS	Q6usq3 valeriana e	1081	79	5.7	453	2	Q8YBB8 LISMO	Q8ybb8 lisimicrobacter
1009	79.5	5.7	677	2	Q6CY48 KLUOLA	Q6cy48 kluveromyces	1082	79	5.7	456	2	Q9HIDS5 THEACI	Q9hds5 thermoplasma
1010	79.5	5.7	695	2	Q9TjS9 9E0NT	Q9tjs9 musaenda a	1083	79	5.7	456	2	Q7PB27 RICHTS8	Q7pb27 richettsia
1011	79.5	5.7	697	1	HAK4 ORYSA	Q6ysas oryza sativ	1084	79	5.7	457	2	Q4N1S2 THEPA	Q4n1s2 thelleria p
1012	79.5	5.7	699	2	Q91L7 MOUSE	Q91l7 mus musculus	1085	79	5.7	457	2	Q3BEP6 9FALC	Q3beb6 spizellomyces
1013	79.5	5.7	726	2	Q22K71 CHLSA	Q2zk71 caldicellul	1086	79	5.7	464	2	Q8RC72 THETN	Q8rc72 thermoanaerobacter
1014	79.5	5.7	733	2	Q44KZ0 CIRSL	Q44kz0 chromohalob	1087	79	5.7	465	2	Q440N7 SOLJS	Q440n7 solis
1015	79.5	5.7	734	2	Q4RNIS7 TETNG	Q4rnis7 tetraodon n	1088	79	5.7	473	2	Q2QWH8 9RYSA	Q2qwh8 oryzasativ
1016	79.5	5.7	735	2	Q4DAB4 TRYCR	Q4dab4 trypanosoma	1089	79	5.7	477	2	Q16252 CABEI	Q16252 caenorhabdobi
1017	79.5	5.7	741	2	Q32132 9E0STR	Q32132 chryanthem	1090	79	5.7	477	2	Q3NNWB3 9GAMM	Q3nnwb3 caenorhabdobi
1018	79.5	5.7	731	1	SL9A3 RAT	SL9a3 rat	1091	79	5.7	481	2	Q62EY5 BURNA	Q62ey5 burkhholderi
1019	79.5	5.7	726	2	Q22K71 CHLSA	Q2zk71 caldicellul	1092	79	5.7	481	2	Q440N7 SOLJS	Q440n7 solis
1020	79.5	5.7	890	2	Q2Y5X4 NTIMU	Q2y5x4 nitrosospir	1093	79	5.7	489	2	Q97EE9 CLOAB	Q97ee9 clostridium
1021	79.5	5.7	976	2	Q96V04 BIUGR	Q96v04 blumeria gr	1094	79	5.7	491	2	Q4KH41 PSEF5	Q4kh41 pseudomonas
1022	79.5	5.7	1078	2	Q55F45 DCDI	Q55f45 dictyosteli	1095	79	5.7	492	2	Q5A405 CANAL	Q5a405 candida alb
1023	79.5	5.7	1163	2	Q2UDG2 ASPOR	Q2udg2 aspergillus	1096	79	5.7	497	2	Q7TNN9 RAT	Q7tnn9 ratitomyces
1024	79.5	5.7	1321	1	Q4RSU1 ERERRW	Q4rsu1 tetradon n	1097	79	5.7	498	2	Q4X148 ASPFU	Q4x148 aspergillus
1025	79.5	5.7	1529	2	Q5H09 DROME	Q5h09 drosophila	1098	79	5.7	501	2	Q5TMB6 GALIUS	Q5tmb6 galillus galli
1026	79.5	5.7	1539	2	Q4UB92 THEIAN	Q4ub92 theleria a	1099	79	5.7	517	2	Q9XYB3 DICDI	Q9xyb3 dictyosteli
1027	79.5	5.7	1569	2	Q5FFEL3 ERERRW	Q5ffel3 erlichia r	1100	79	5.7	518	2	Q3CGR2 THEET	Q3cgr2 thermoanaerobacter
1028	79.5	5.7	1591	2	Q5FFEL3 ERERRW	Q5ffel3 erlichia r	1101	79	5.7	524	2	Q4W1S8 ASPFU	Q4w1s8 aspergillus
1029	79.5	5.7	154	2	Q42211 NFMCA	Q42211 necurus ma	1102	79	5.7	526	2	Q4J830 SULAC	Q4j830 sulfolobus
1030	79.5	5.7	172	1	NUM6 PETINA	Num6 petromyzon	1103	79	5.7	534	2	Q88Z37 LACTOBACILLI	Q88z37 lactobacilli
1031	79.5	5.7	183	1	Y507 HAETIN	Y507 haemophilus	1104	79	5.7	545	2	Q5P5X2 9BRAD	Q5p5x2 bradyrhizobium
1032	79.5	5.7	183	2	Q40N39 HAE18	Q40n39 haemophilus	1105	79	5.7	551	2	Q41G2 DESHA	Q41g2 desulfobacter
1033	79.5	5.7	192	2	Q6CYK5 ERWCT	Q6cyk5 erwinia car	1106	79	5.7	585	2	Q60UUI1 CAEBR	Q60uui1 caenorhabdobi
1034	79.5	5.7	226	2	Q6HCD0 BACHK	Q6hcd0 bacillus th	1107	79	5.7	595	2	Q37TQ4 ENTFA	Q37tq4 enterococcus
1035	79.5	5.7	229	2	Q8X1K9 CIPOE	Q8x1k9 clostridium	1108	79	5.7	602	2	Q70X1B 9METTA	Q70x1b mettles
1036	79.5	5.7	248	2	Q5OEH3 LACRE	Q5oeh3 lactobacill	1109	79	5.7	657	2	Q3SUK6 NITWN	Q3suk6 nitrobacter
1037	79.5	5.7	269	2	Q3QSB7 9RHOB	Q3qsb7 silicibacte	1110	79	5.7	658	2	Q6XJH8 9ERIC	Q6xjh8 sideroxydol
1038	79.5	5.7	278	2	Q5K125 POPULUS	Q5k125 populus tre	1111	79	5.7	658	2	Q421G2 DESHA	Q421g2 desulfobacter
1039	79.5	5.7	282	2	Q4ULV8 PICKETTSIA	Q4ulv8 pickettsia	1112	79	5.7	688	2	Q6XJ12 9BORA	Q6xj12 sideroxydol
1040	79.5	5.7	289	2	Q946J9 MEDICAGO	Q946j9 medicago tr	1113	79	5.7	692	2	Q9TIIW2 9ASTE	Q9tiiw2 phaeelia ca
1041	79.5	5.7	289	2	Q5U710 9FABA	Q5u710 glycyrrhiza	1114	79	5.7	693	1	Q69U14 ORYSA	Q69u14 oryzasativ
1042	79.5	5.7	293	1	Y543 CHLPN	Q9s809 glomandra p	1115	79	5.7	695	2	Q19822 ALSOBIA	Q19822 alsobia sp
1043	79.5	5.7	293	2	Q9KD25 BACHD	Q9kd25 bacillus ha	1116	79	5.7	697	2	Q3HT37 9BORA	Q3ht37 tiquilia hi
1044	79.5	5.7	300	2	Q6HM61 BACHK	Q6hm61 bacillus th	1117	79	5.7	697	2	Q3HT35 9BORA	Q3ht35 tiquilia hi
1045	79.5	5.7	307	2	Q9UTQ9 NEILMA	Q9utq9 neisseria m	1118	79	5.7	698	2	Q8M8X1 SPHENOCLEA	Q8m8x1 sphenoclea
1046	79.5	5.7	310	2	Q7M0J1 VEBV	Q7m0j1 vibrio vuln	1119	79	5.7	699	2	Q9TIIW2 9ASTE	Q9tiiw2 phaeelia ca
1047	79.5	5.7	320	2	Q8DAH5 VEBV	Q8dah5 vibrio vuln	1120	79	5.7	700	2	Q5193 9MOUSE	Q5193 morula cit
1048	79.5	5.7	341	2	Q5P1X1 A20SE	Q5p1x1 azoarcus sp	1122	79	5.7	700	2	Q9TIIW7 DIGPU	Q9tiiw7 digitalis p
1049	79.5	5.7	341	2	Q2QWHT ORISA	Q2qwh7 oryzasativ	1123	79	5.7	704	2	Q4023 DESULFUR	Q4023 desulfurobacter
1050	79.5	5.7	345	2	Q97C19 THEVO	Q97c19 thermoplasm	1124	79	5.7	708	2	Q10R23 DESACU	Q10r23 bacillus su
1051	79.5	5.7	369	2	Q8PL40 XANAC	Q8pl40 xanthomonas	1125	79	5.7	830	2	Q2V621 CANAL	Q2v621 canal
1052	79.5	5.7	372	2	Q6GIA8 STAR	Q6gia8 staphylococ	1126	79	5.7	837	2	Q8LBH3 ARATH	Q8lbh3 arabidopsis
1053	79.5	5.7	373	2	Q8LBH3 ARATH	Q8lbh3 arabidopsis	1127	79	5.7	904	2	Q2X4H3 9GAMM	Q2x4h3 gammaproteobacter

1127	5.7	1067	2	Q3Q8Y9_9GAMM	shewanella	Q3g8y9	2	Q4QK73_HAEI8	haemophilus	Q4qk73	2
1128	5.7	1068	2	Q2ZN8_SHEPU	shewanella	Q2zn8	2	Q49vd5_STAS1	staphylococcus	Q49vd5	2
1129	5.7	1166	2	Q44EN7_CIRSL	aspergillus	Q44en7	2	Q5AY52_EMEN1	aspergillus	Q5ay52	2
1130	5.7	1166	2	Q8CTQ9_MOUSE	chromobacter	Q8ctq9	2	Q5GCAB_RHOGE	rhodococcus	Q5gcab	2
1131	5.7	1501	2	Q3TDN0_MOUSE	mus musculu	Q3tdn0	2	Q8AQ0_COXBU	corynebacterium	Q8aq0	2
1132	5.7	1521	2	Q3UJL8_MOUSE	mus musculu	Q3ujl8	2	Q85MF7_9NEOP	cysteatis th	Q85mf7	2
1133	5.7	1521	2	Q80ZB8_MOUSE	mus musculu	Q80zb8	2	Q2LB19_9NEOP	thauria ali	Q2lb19	2
1134	5.7	1521	2	Q8CGS3_MOUSE	mus musculu	Q8cgs3	2	Q3ZEP8_SP1FL	epidermophytes	Q3zep8	2
1135	5.7	1521	2	Q8CIP6_MOUSE	mus musculu	Q8cip6	2	Q9v0T0_PYRAB	pyrococcus	Q9v0t0	2
1136	5.7	1709	2	Q61IW5_CAEBR	caenorhabdi	Q61iw5	2	Q8FB10_ECOL6	escherichia	Q8fb10	2
1137	5.7	1794	2	Q4QV5_LBIMA	leishmania	Q4qv5	2	Q3GYP4_LACTO	lactobacillus	Q3gyp4	2
1138	5.7	2198	2	Q18950_CAEEL	caenorhabdi	Q18950	2	Q3ICQ3_PSEHT	pseudoalter	Q3icq3	2
1139	5.6	169	2	Q9H8A7_HALSA	halobacteri	Q9hsa7	2	Q9B8Y2_FASHE	fasciola he	Q9b8y2	2
1140	5.6	182	2	Q3CSM3_ALTAT	pseudodalter	Q3sm3	2	Q6ZMD2_HUMAN	homo sapiens	Q6zmd2	2
1141	5.6	188	2	Q43ZW3_BLOPB	blochmannia	Q43zw3	2	Q3VHK6_9SPHN	sphingopyxis	Q3vhk6	2
1142	5.6	241	1	MCB6_ECOLI	escherichia	P0528	2	Q6mbu7_MYCM5	mycoplasma	Q6mbu7	2
1143	5.6	242	2	Q6LP6_PRDPR	photobacter	Q6lp6	2	Q2U3B4_ASPOR	sporobacter	Q2u3b4	2
1144	5.6	247	2	Q3B7R3_BARE	brachydano	Q3b7r3	2	Q2W3Z5_MAGS5	magnospir	Q2w3z5	2
1145	5.6	254	2	Q4SVF4_TETING	tetradon n	Q4svf4	2	Q6DCE3_XENLA	xenopus lae	Q6dce3	2
1146	5.6	259	2	Q3CMD0_ALTAT	pseudodalter	Q3cmd0	2	Q3SN0N5_RALME	ralstonia m	Q3sn0n5	2
1147	5.6	264	2	Q6ITH4_CERBA	cercaria ba	Q6ith4	2	Q50465_MYCUT	mycobacteri	Q50465	2
1148	5.6	264	2	Q6IT12_CERBA	cercaria ba	Q6it12	2	Q4MPJB8_BACCE	bacillus ce	Q4mpjb8	2
1149	5.6	281	2	Q5J7T1_PTKAR	pyrococcus	Q5j7t1	2	Q950T2_HYACU	hyaloraphis	Q950t2	2
1150	5.6	293	2	Q4W8S1_9ACAR	leptorombi	Q4w8s1	2	Q8SXJ9_DROMB	drosophila	Q8sxj9	2
1151	5.6	298	2	Q65V25_MANSM	mannheimia	Q65v25	2	Q979U1_DROME	uncultured	Q979u1	2
1152	5.6	298	2	Q73T54_MCPA	mycobacteri	Q73t54	2	Q2X4Y6_DARCH	uncultured	Q2x4y6	2
1153	5.6	302	2	Q4LB8C2_STAHJ	staphylococ	Q4lb8c2	2	Q2TK00_9ERIC	uncultured	Q2tk00	2
1154	5.6	314	2	Q970C7_SULITO	sulfolobus	Q970c7	2	Q1221_BRACU	bacillus su	Q1221	2
1155	5.6	316	2	Q7EV23_ORVSA	oryza sativ	Q7ev23	2	Q1JYR6_ARATH	arabidopsis	Q1jyr6	2
1156	5.6	320	2	Q9BV64_9MVRT	warneckea m	Q9bv64	2	Q3VQ16_BRANL	brassica na	Q3vq16	2
1157	5.6	320	2	Q72NB59_XENLA	xenopus lae	Q72nb59	2	Q5Nm95_ZYMMO	zymomonas m	Q5nm95	2
1158	5.6	321	2	Q9BBV9_9MVRT	muriori hel	Q9bbv9	2	Q97IX1_CODON	schen	Q97ix1	2
1159	5.6	324	2	Q2IVYA_RHOPA	rhodospseudoo	Q2iva0	2	Q6USQ0_9DIPS	roglera sur	Q6usq0	2
1160	5.6	324	2	Q970C7_STLITO	sulfolobus	Q970c7	2	Q3H46_TIQUILIA	tiquilia gr	Q3h46	2
1161	5.6	325	2	Q7EV23_ORVSA	oryza sativ	Q7ev23	2	Q3JYR5_BRANA	brassica na	Q3jyr5	2
1162	5.6	330	2	Q9V0D4_DROMB	drospohila	Q9v0d4	2	Q2LYT2_DROPS	drosophila	Q2lyt2	2
1163	5.6	333	2	Q3DR8T7_STRAG	streptococc	Q3dr8t7	2	Q870T0_9GENT	uncultured	Q870t0	2
1164	5.6	333	2	Q3DB03_STRA4	streptococc	Q3db03	2	Q9NJP6_9GENT	uncultured	Q9njp6	2
1165	5.6	333	2	Q3K087_STRA1	streptococc	Q3k087	2	Q23645_MENTR	mentibacter	Q23645	2
1166	5.6	340	2	Q5P46_NF1G1	neisseria g	Q5p46	2	Q3H46_9BORA	uncultured	Q3h46	2
1167	5.6	325	2	Q9MR21_9MVRT	heterocentri	Q9mr21	2	Q3JYR5_BRANA	brassica na	Q3jyr5	2
1168	5.6	330	2	Q9V0D4_DROMB	drospohila	Q9v0d4	2	Q2LYT2_DROPS	drosophila	Q2lyt2	2
1169	5.6	333	2	Q3DR8T7_STRAG	streptococc	Q3dr8t7	2	Q870T0_9DELTA	uncultured	Q870t0	2
1170	5.6	333	2	Q3DB03_STRA4	streptococc	Q3db03	2	Q9NJP6_9GENT	uncultured	Q9njp6	2
1171	5.6	324	2	Q5P46_NF1G1	neisseria g	Q5p46	2	Q23645_MENTR	mentibacter	Q23645	2
1172	5.6	340	2	Q8GB45_BIFLU	bifidobacte	Q8gb45	2	Q1239_BRACU	uncultured	Q1239	2
1173	5.6	356	2	Q8DTM2_SPMU2	streptococc	Q8dtm2	2	Q1240_BRACU	uncultured	Q1240	2
1174	5.6	362	2	Q3R3B4_XLIFA	xylella fas	Q3r3b4	2	Q1241_BRACU	uncultured	Q1241	2
1175	5.6	366	1	Y1196_MEJUA	methanococc	Y1196	2	Q1242_BRACU	uncultured	Q1242	2
1176	5.6	384	2	Q3CNM8_ALTAT	pseudodalter	Q3cnm8	2	Q1243_BRACU	uncultured	Q1243	2
1177	5.6	389	2	Q4ZNB3_PSU02	pseudomonas	Q4znb3	2	Q1244_BRACU	uncultured	Q1244	2
1178	5.6	340	2	Q93TD9_PSYM	pseudomonas	Q93td9	2	Q1245_BRACU	uncultured	Q1245	2
1179	5.6	389	2	Q87ND8_PESM2	pseudomonas	Q87nd8	2	Q1246_BRACU	uncultured	Q1246	2
1180	5.6	393	2	Q63NR7_BAC22	bacteroides	Q63nr7	2	Q1247_BRACU	uncultured	Q1247	2
1181	5.6	395	2	Q612T3_CAEBR	caenorhabdi	Q612t3	2	Q1248_BRACU	uncultured	Q1248	2
1182	5.6	397	2	Q8KBW37_RUEGERIA	ruegeria sp	Q8kbw37	2	Q1249_BRACU	uncultured	Q1249	2
1183	5.6	397	2	Q5NHJ1_FRAOTT	francisella	Q5nhj1	2	Q1250_BRACU	uncultured	Q1250	2
1184	5.6	405	2	Q9U2M5_CAEEL	caenorhabdi	Q9u2m5	2	Q1251_BRACU	uncultured	Q1251	2
1185	5.6	414	2	Q4CMW9_TRICR	trypanosoma	Q4cmw9	2	Q1252_BRACU	uncultured	Q1252	2
1186	5.6	419	2	Q3P1D7_9GAMM	staphylococ	Q3p1d7	2	Q1253_BRACU	uncultured	Q1253	2
1187	5.6	436	2	Q4K6F5_PSEF5	cyanobacter	Q4k6f5	2	Q1254_BRACU	uncultured	Q1254	2
1188	5.6	437	2	Q31IW2_THICR	thiomicrosp	Q31iw2	2	Q1255_BRACU	uncultured	Q1255	2
1189	5.6	438	2	Q4B1S3_PSEB14	pseudomonas	Q4b1s3	2	Q1256_BRACU	uncultured	Q1256	2
1190	5.6	442	2	Q2L207_BORAV	bordeiella	Q2l207	2	Q1257_BRACU	uncultured	Q1257	2
1191	5.6	443	2	Q82JL4_SALCH	salmonella	Q82jl4	2	Q1258_BRACU	uncultured	Q1258	2
1192	5.6	443	2	Q892C7_BACTIN	bacteroides	Q892c7	2	Q1259_BRACU	uncultured	Q1259	2
1193	5.6	447	2	Q2MG78_STPAU	thiomicrosp	Q2mg78	2	Q1260_BRACU	uncultured	Q1260	2
1194	5.6	457	2	Q7A856_STPAU	staphylococ	Q7a856	2	Q1261_BRACU	uncultured	Q1261	2
1195	5.6	464	2	Q992A4_STAMM	staphylococ	Q992a4	2	Q1262_BRACU	uncultured	Q1262	2
1196	5.6	470	2	Q6C8J1_YARILLI	thermoplasm	Q6c8j1	2	Q1263_BRACU	uncultured	Q1263	2
1197	5.6	470	2	Q31KWO_SNTP7	erwinia car	Q31kwo	2	Q1264_BRACU	uncultured	Q1264	2
1198	5.6	470	2	Q5NI09_SNTP6	synochococc	Q5ni09	2	Q1265_BRACU	uncultured	Q1265	2
1199	5.6	471	2	Q6AB86_PROAC	propionibac	Q6ab86	2	Q1266_BRACU	uncultured	Q1266	2

1273	78	Q7S3I4_NEUCR	neurospora	Q8E9A7_SHEON	shewanella
1274	78	Q8QWJ7_METNA	methanosaer	Q9K223_RHIBET	rhabdium e
1275	78	Q3CEJ9_THEET	thermoaer	Q4vn69_PLABE	plasmobium
1276	78	Q65f48_BACLD	bacillus li	Q4gexi_leIMIA	leishmania
1277	78	Q85169_9TREM	chimaerohem	Q5ky19_gebacillus	gebacillus
1278	78	Q921S9_RICCN	rickettsia	Q9ka14_bacillus_ha	bacillus ha
1279	78	Q5PIK0_AZORES	azores sp	Q5uqj2_minivirus	minivirus
1280	78	Q9rt25_DEINOCOCCUS	deinococcus	Q93rc4_ecoli	escherichia
1281	78	Q9PSM5_BAT	rattus norv	Q3hi18_trichodesmi	trichodesmi
1282	78	Q57mb7_SALCH	salmonella	Q3vhj8_pelodictyon	pelodictyon
1283	78	Q5PBP30_SALPA	salmonella	Q3IDA4_pselaoder	pselaoder
1284	78	Q82N77_SALTY	salmonella	Q7vv38_bordetella	bordetella
1285	78	Q82581_BALTII	salmonella	Q7w0u7_bordetella	bordetella
1286	78	Q81RH3_BACAN	bacillus an	Q7wn67_bordetella	bordetella
1287	78	Q35xx3_MOUSE	mus musculu	Q8ub2b7_pyrococcus	pyrococcus
1288	78	Q6HZP9_BACAN	bacillus an	Q4cxm5_trycr	trypanosoma
1289	78	Q6hQ07_BACHK	bacillus th	Q92wh1_rhizobium_m	rhizobium m
1290	78	KCMK3_RAT	rattus norv	Q6njG1_corynebacte	corynebacte
1291	78	YMB7_YEAST	rattus norv	Q9mf61_beia	beia
1292	78	Q35xx3_MOUSE	shewanella	Q7w0u7_BORPA	BORPA
1293	78	QXLR_MOUSE	shewanella	Q7wn67_BORPA	BORPA
1294	78	Q5f1R6_LACAC	staphyloc	Q8uB08_SYNNS9	synchococc
1295	78	Q22672_CABECT	caenorhabdi	Q4hpk2_camplobact	campylobact
1296	78	Q6S7Z8_9BACT	caenorhabdi	Q6asd9_desps	desulfovib
1297	78	Q421Y0_DBSHA	desulfobacto	Q4ek11_listeria	listeria mo
1298	78	Q6L334_PPROJ	desulfobacter	Q8y8n6_listeria	listeria mo
1299	78	Q41ab4_STAHU	desulfobacter	Q721v7_listeria	listeria mo
1300	78	Q41HS6_CMCMO	desulfobacter	Q2xbL5_psBpu	psedomonas
1301	78	Q4HV12_CMLMA	desulfobact	Q4HPK2_CAMUP	camylobact
1302	78	Q7vaq3_PROMA	desulfobact	Q6asd9_cordi	desulfovib
1303	78	Q3BEN3_9PALC	desulfobacto	Q4ek11_lisimo	lisimo
1304	78	Q918L1_PRFU	desulfobacter	Q721v7_lisimo	lisimo
1305	78	Q95jd3_RABBIT	desulfobacter	Q2Jx36_9CYAN	cyanobacter
1306	78	Q3JCK0_NUTOC	desulfobacter	Q31u75_SHIBS	shigella bo
1307	78	Q3XX38_ENTFC	desulfobact	Q660j1_borreli	borreli ga
1308	78	Q8GGM7_STRAZ	desulfobact	Q7tr57_MOUSE	mus musculu
1309	78	Q2WYTS7_9GAMM	desulfobact	Q8vg20_MOUSE	mus musculu
1310	78	Q33323_METHU	desulfobact	Q7Ts53_MOUSE	mus musculu
1311	78	Q8EK6_SEBON	desulfobact	Q8rfj5_fusobacteri	fusobacteri
1312	78	Q687i4_MOUSE	desulfobact	Q70rw1_beardius	b
1313	78	Q8FP18_COREF	desulfobact	Q94vc3_varanus	varanus ruf
1314	78	Q6R9J4_MALIZ	desulfobact	Q01m15_TARRU	tarru
1315	78	Q8BYVS0_MOUSE	desulfobact	Q2utw7_aspergilus	aspergilus
1316	78	Q2JD90_9TIAN	desulfobact	Q4vz3_trypansoma	trypansoma
1317	78	Q9B122_RHILLO	desulfobact	Q6gds8_staphyloc	staphyloc
1318	78	Q3QF78_9GAMM	desulfobact	Q9yfu4_aecopyrum	aecopyrum p
1319	78	Q6f8p4_deCIAR	desulfobact	Q3d2e9_traptoccc	traptoccc
1320	78	Q35IA8_9RAD	desulfobact	Q9x0n3_themotoga	themotoga
1321	78	Q3Jx86_BLRP1	desulfobact	Q70rw1_9CETTA	9CETTA
1322	78	Q9JAB1_9TIAN	desulfobact	Q2utw7_aspor	aspor
1323	78	Q54IV7_DCDI	desulfobact	Q4d715_trycr	trycr
1324	78	Q3QF78_9GAMM	desulfobact	Q8FV3_9TRYP	tryptophan
1325	78	Q47884_DICAR	desulfobact	Q6GDS8_STAAR	staar
1326	78	Q35IA8_9RAD	desulfobact	Q9yfu4_aeropyrum	aeropyrum p
1327	78	Q3Jx86_BLRP1	desulfobact	Q3d2e9_strag	strag
1328	78	Q9JAB1_9TIAN	desulfobact	Q9x0n3_thema	thema
1329	78	Q54IV7_DCDI	desulfobact	Q70rw1_9CETTA	9CETTA
1330	78	Q8BVG6_MOUSE	desulfobact	Q2utw7_aspor	aspor
1331	78	Q6CQ66_KLILA	desulfobact	Q4vz3_trypansoma	trypansoma
1332	78	Q34FM4_RHOPIA	desulfobact	Q6gds8_staphyloc	staphyloc
1333	78	Q5NAP5_RHOPIA	desulfobact	Q9xmu9_tetrhyrema	tetrhyrema
1334	78	Q46TV6_METBA	desulfobact	Q33tm7_brachydano	brachydano
1335	78	Q59RNO_CANAL	desulfobact	Q57pc1_salmoneella	salmoneella
1336	78	Q9FIS8_RHOPIA	desulfobact	Q978i2_thermoplasma	thermoplasma
1337	78	Q42L77_PSEU2	desulfobact	Q4nij1_mic	mic
1338	78	Q01843_CABEL	desulfobact	Q2urz0_aspergillus	aspergillus
1339	78	Q8P2F8_LIPIC	desulfobact	Q4Jz96_streptococ	streptococ
1340	78	Q59TM8_CANAL	desulfobact	Q3gkda4_prosthecoch	prosthecoch
1341	78	Q59TR0_CANAL	desulfobact	Q6p6x7_thiobacillu	thiobacillu
1342	78	Q59TR0_CANAL	desulfobact	Q33tm7_shewanella	shewanella
1343	78	Q59TR0_CANAL	desulfobact	Q57pc1_salmoneella	salmoneella
1344	78	Q59TR0_CANAL	desulfobact	Q978i2_thermoplasma	thermoplasma
1345	78	Q59TR0_CANAL	desulfobact	Q4nij1_mic	mic
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1347	78	Q9K223_RHIBET	rhabdium e	Q9xmu9_tetrhyrema	tetrhyrema
1348	78	Q4vn69_PLABE	plasmobium	Q3gkda4_prosthecoch	prosthecoch
1349	78	Q4gexi_leIMIA	leishmania	Q6p6x7_brachydano	brachydano
1350	78	Q5ky19_gebacillus	gebacillus	Q33tm7_shewanella	shewanella
1351	78	Q9ka14_bacillus_ha	bacillus ha	Q57pc1_salmoneella	salmoneella
1352	78	Q9uqj2_minivirus	minivirus	Q978i2_thermoplasma	thermoplasma
1353	78	Q93rc4_ecoli	escherichia	Q4nij1_mic	mic
1354	78	Q3hi18_trichodesmi	trichodesmi	Q2urz0_aspergillus	aspergillus
1355	78	Q3vhj8_pelodictyon	pelodictyon	Q4Jz96_streptococ	streptococ
1356	78	Q3IDA4_pselaoder	pselaoder	Q9xmu9_tetrhyrema	tetrhyrema
1357	78	Q7vv38_bordetella	bordetella	Q3gkda4_prosthecoch	prosthecoch
1358	78	Q7w0u7_bordetella	bordetella	Q6p6x7_brachydano	brachydano
1359	78	Q7wn67_bordetella	bordetella	Q33tm7_shewanella	shewanella
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1361	78	Q8v8n6_listeria	listeria mo	Q978i2_thermoplasma	thermoplasma
1362	78	Q8y8n6_listeria	listeria mo	Q4nij1_mic	mic
1363	78	Q8zr57_mycobact	mycobact	Q4Jz96_streptococ	streptococ
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1365	78	Q8zb08_synchococc	synchococc	Q33tm7_shewanella	shewanella
1366	78	Q8ze98_psedomonas	psedomonas	Q57pc1_salmoneella	salmoneella
1367	78	Q8zf57_campylobact	campylobact	Q978i2_thermoplasma	thermoplasma
1368	78	Q8zgvs5_yerpes	yerpes	Q4nij1_mic	mic
1369	78	Q8zgvs5_yerpes	yerpes	Q4nij1_mic	mic
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1371	78	Q8zgvs5_yerpes	yerpes	Q4nij1_mic	mic
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1413	78	Q8zgvs5_yerpes	yerpes	Q4nij1_mic	mic
1414	78	Q8zgvs5_yerpes	yerpes	Q4nij1_mic	mic
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1418	78	Q8zgvs5_yerpes	yerpes	Q4nij1_mic	mic

1419	5.6	477	2	Q7MKV7_VIBVY	Q7mkv7 vibrio vuln	1492	77	5.5	269	2	Q73K03_TREDE
1420	5.6	477	2	Q8DPF8_VIBPA	Q8dpf8 vibrio para	1493	77	5.5	271	2	Q46dvs5_methanobarc
1421	5.6	477	2	Q8D911_VIBVU	Q8d911 vibrio para	1494	77	5.5	274	2	Q59kp1_candida alb
1422	5.6	477	2	Q7AE73_ECO57	Q7ae73 escherichia	1495	77	5.5	277	2	Q4mnw5_baccae
1423	5.6	479	2	Q3QNW1_9RHOB	Q3qnw1 silicibacte	1496	77	5.5	277	2	Q73006_BACCI
1424	5.6	481	2	Q2S053_9GAMM	Q2s053 haelli che	1497	77	5.5	282	2	Q4egi7_listeria mo
1425	5.6	482	2	Q5KYK3_GROKA	Q5kyk3 geobacillus	1498	77	5.5	282	2	Q4epa3_listeria mo
1426	5.6	483	2	Q2U058_ASPOR	Q2u058 aspergillus	1499	77	5.5	282	2	Q720H2_LISMO
1427	5.6	484	2	Q4CDFC2_CLDMT	Q4dcf2 clostridium	1500	77	5.5	282	2	Q87ym2_listeria mo
1428	5.6	492	2	Q7VPNT5_HELHP	Q7vpnt5 helicobacte						
1429	5.6	499	2	Q5JU20_SALUCH	Q5ju20 salmonella						
1430	5.6	499	2	Q82353_SALUTI	Q823s3 salmonella						
1431	5.6	500	2	Q2KS546_RHEBT	Q2ks546 rhizobium e						
1432	5.6	504	2	Q68816_ORVSA	Q68816 oryza sativ						
1433	5.6	507	2	Q7VSQ9_BORP8	Q7vsq9 bordelella						
1434	5.6	507	2	Q7WHD8_BORBR	Q7whd8 bordelella						
1435	5.6	510	2	Y382_RICPRH	Y382 rickettsia						
1436	5.6	510	2	Q9LLE20_ARATH	Q9le20 arabidopsis						
1437	5.6	510	2	Q4MXE6_BACCE	Q4mx86 bacillus ce						
1438	5.6	513	2	Q9KG54_VLECH	Q9kl84 vibrio chol						
1439	5.6	520	2	Q32477_JUSAM	Q32477 justicia am						
1440	5.6	524	2	Q45869_9BURK	Q458g9 burkholderi						
1441	5.6	524	2	Q4LPY5_9BURK	Q4lpv5 burkholderi						
1442	5.6	526	1	STP13_ARATH	Q9azz2 arabidopsis						
1443	5.6	526	2	Q55NR7_CRTNE	Q5wr7 cryptococcus						
1444	5.6	526	2	Q5KU10_CRINE	Q5kj10 cryptococcus						
1445	5.6	527	2	Q5ATG4_EMENTI	Q5at94 aspergillus						
1446	5.6	531	2	Q6YQ13_ONYPE	Q6yq13 onion yellow						
1447	5.6	532	2	C0X1_RHOCA	P9059 rhodobacter						
1448	5.6	532	2	Q40H04_9RHOB	Q40hu4 jannaschia						
1449	5.6	532	2	Q55577_SNXY3	Q55577 synechocyst						
1450	5.6	535	2	Q43ZK5_SOJUS	Q4zks5 solibacter						
1451	5.6	612	2	Q76H61_KATPVE	Q76h61 katuwonus						
1452	5.6	612	2	Q85U51_9SCOM	Q85u51 euthynus a						
1453	5.6	612	2	Q3XH94_9PROT	Q3xh94 magnetococc						
1454	5.6	617	2	Q7S080_NEUCR	Q7s080 neurospora						
1455	5.6	630	1	SC6A4_MACMU	Q9nyx0 macaca mulu						
1456	5.6	633	2	Q9ASS7_ARATH	Q9ass7 rabidobiposis						
1457	5.6	633	2	Q8L616_PESOC	Q8l616 pisaster oc						
1458	5.6	643	2	Q385G4_9TRYP	Q385g4 trypanosoma						
1459	5.6	648	2	Q8SLR2_COUGU	Q8slr2 couroupita						
1460	5.6	649	2	Q28439_ARCPE	Q28449 archaeoglob						
1461	5.6	660	2	Q6YLT3_9ILLII	Q6ylt3 lachnanthes						
1462	5.6	665	2	Q9GG79_9POAL	Q9gg79 dulichium a						
1463	5.6	695	2	Q9TA18_THEPO	Q9ta18 thermoplasm						
1464	5.6	698	2	Q6BG72_DEBHA	Q6bg72 debaryomyce						
1465	5.6	698	2	Q7YN04_9SOLIA	Q7yn04 metternichia						
1466	5.6	706	2	Q6MK05_BDBBA	Q6mk05 bdellobiviri						
1467	5.6	706	2	PAL2_ARATH	P4724 arabidopsis						
1468	5.6	750	2	Q93SS0_XANCP	Q93ss9 xanthomonas						
1469	5.6	776	2	Q61N50_CABRR	Q61nz0 caenothabdi						
1470	5.6	821	2	Q4CY87_TRYCR	Q4cy87 trypanosoma						
1471	5.6	839	2	Q8TQ74_METACO	Q8tq74 methanosa						
1472	5.6	855	2	Q75A19_ASPGO	Q75av9 ashbya gross						
1473	5.6	861	2	Q89FM4_BRAJA	Q8bfw4 bradyrhizob						
1474	5.6	870	1	GP155_HUMAN	Q733f1 homo sapien						
1475	5.6	870	2	Q4G076_HUMAN	Q4g076 homo sapien						
1476	5.6	877	2	Q2SB79_9GAMM	Q2sb79 haelli che						
1477	5.6	881	2	Q3IL61_PSEHT	Q3il61 pseudalter						
1478	5.6	945	1	SYI_ACIAID	Q6f902 acinetobact						
1479	5.6	953	1	CWH43_YEAST	P2618 saccharomyces						
1480	5.6	1069	2	Q4IVN6_AZOVI	Q4ivva6 azotobacter						
1481	5.6	1118	2	Q9HUE7_PSEAH	Q9auer pseudomonas						
1482	5.6	1402	1	K0232_HUMAN	Q232 homolog						
1483	5.6	1551	2	Q44718_SOJUS	Q44718 solibacter						
1484	5.6	1646	2	Q5B005_EMENI	Q5b005 aspergillus						
1485	5.6	175	1	Q3A0L5_PELUD	Q3a0l5 pelobacter						
1486	5.6	181	2	Q8ZD94_PYRAE	Q8zdu94 pyrobaculum						
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1488	5.6	262	2	Q8KJ77_RHIO	Q8kj77 rhizobacter						
1489	5.6	268	2	Q35LM3_9BRAD	Q35lm3 bradyrhizob						
1490	5.6	269	2	Q4BB89_BURVI	Q4bb89 burkholderi						
1491	5.6	269	2	Q393M5_BURS3	Q393m5 burkholderi						

RESULT 1 HUMAN

SEQUENCE

Nucleotide sequence

NCBI TaxID: 9606

RN

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX35892; AAQ88956.1; mRNA.

DR EMBL; BC047025; AAH47025.3; mRNA.

DR EMBL; BC058116; CAI19266.1; Genomic_DNA.

DR EMBL; BC091509; AAH91509.1; mRNA.

DR Ensembl; ENSSG00000156171; Homo sapiens.

KW Hypothetical Protein.

SEQUENCE 266 AA; 29766 MW; 4F91D5C212D458E5 CRC64;

Query Match Score 1392; DB 2; Length 266;

Best Local Similarity 100.0%; Pred No. 6e-108; Matches 0; Indels 0; Gaps 0;

Matches 266; Conservative 0; Mismatches 0; Del 0; Insert 0; GapOpen 0; GapClose 0;

QY 1 MWNFQQISFLPSALVIWTAARIFSYITAVTLLHIDPALPYISDTGTVAPEKCLFGAML 60

DB 1 MWNFQQISFLPSALVIWTAARIFSYITAVTLLHIDPALPYISDTGTVAPEKCLFGAML 60

QY 61 NIAAVLCLATTIVRYKQVHALSPENVTKLNKAGLVIGLSCUGLSIVANFQKTLFPA 120

DB 61 NIAAVLCLATTIVRYKQVHALSPENVTKLNKAGLVIGLSCUGLSIVANFQKTLFPA 120

QY 121 HVSGAVLTFGMSLYMFVOTILSYQMOKRHKQVFWIRLLIVWCGVSAISMLTCSSVL 180

DB 121 HVSGAVLTFGMSLYMFVOTILSYQMOKRHKQVFWIRLLIVWCGVSAISMLTCSSVL 180

QY 1B1 HSGNFGTDLQKLHWNPEDKGKVYLHMTTAENSMSFFGGPFELTYIRDFQKISLRVEAN 240

DB 1B1 HSGNFGTDLQKLHWNPEDKGKVYLHMTTAENSMSFFGGPFELTYIRDFQKISLRVEAN 240

QY 241 LHGLTYDTPCPINNERTLRSIDI 266

DB 241 LHGLTYDTPCPINNERTLRSIDI 266

RESULT 2 Q4YWF6_HUMAN PRELIMINARY; PRT; 266 AA.

ID Q4YWF6;

AC Q4YWF6_HUMAN

RA 05-JUL-2005, integrated into UniProtKB/TREMBL.

DT 05-JUL-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE Putative transmembrane protein.

OS Homo_sapiens_(Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;

OX [1]

RN RP NUCLEOTIDE SEQUENCE.

RC STRATN=Hereford; TISSUE=Rumen;

RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,

RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shemesh C.,

RA Wagner L., Bala M., Barbizuk S., Barber S., Babakirff R., Beland J.,

RA Chun E., Del Rio L., Gibson S., Hansson R., Kirkpatrick R., Liu J.,

RA Matsuo C., Mayo M., Santos R.R., Scott J., Tsai M., Wong D.,

RA Siddiqui A., Holt R., Jones S.J., Marra M.A.,

RA Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.

CC DR EMBL; BC102918; AA102919.1; - mRNA.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE.

RA Thomas D.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE.

RC TISSUE;Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

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[CC]

DR EMBL; AX336747; AR02410.1; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR Transmembrane.

RN Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

OY	181	HSGNFGTDLQKHLWNPDKGTVLHMITTAEWMSFFGGFPFLTYIRDFQKISLRYEAN	240	RA Yamamoto H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
DB	181	YNGSGFAGAIQKLHLWNPDKGTVLHMITTAEWMSFFGGFPFLTYIRDFQKISLRYEAT	240	RA Grimmond S.M., Teasdale R.D., Liu B.T., Brusic V., Quackenbush J.,
OY	241	LHGTLTLYDAPCPNNERTLRLSDI	266	RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
DB	241	LHGTLTLYDAPCPNNERTLRLSDV	266	RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
OY	241	LHGTLTLYDAPCPNNERTLRLSDI	266	RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawashihira N.,
DB	241	LHGTLTLYDAPCPNNERTLRLSDV	266	RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
OY	241	LHGTLTLYDAPCPNNERTLRLSDI	266	RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
DB	241	LHGTLTLYDAPCPNNERTLRLSDV	266	RA Tagami M., Wakai K., Watshiki A., Okumura-Ohno Y., Suzuki H., Kawai J.,
OY	241	LHGTLTLYDAPCPNNERTLRLSDI	266	RA Hayashizaki Y.,
DB	241	LHGTLTLYDAPCPNNERTLRLSDV	266	RA "The transcriptional landscape of the mammalian genome.";
RESULT 4				RT Science 309:1553-1563 (2005).
QCR48 MOUSE		PRELIMINARY	PRT;	267 AA.
ID QCR48				RN RN
AC				RP NUCLEOTIDE SEQUENCE.
DT	01-JUN-2001	integrated into UniProtKB/T-EMBL.		RC STRAIN=NOD, and C57BL/6J; TISSUE=Activated spleen, Mammary gland,
DT	01-JUN-2001	sequence version 1.		RC Tongue, and Whole body/
DT	01-FEB-2006	entry version 20.		RC Tongue, and Whole body;
DE	10 days embryo whole body cDNA	RIKEN full-length enriched library,		RX RX
DE	clone:610318G18 product:hypothetical protein	full insert sequence		PUBMED=16141073; DOI=10.1126/science.1112009;
DE	(Adult male tongue cDNA)	RIKEN full-length enriched library,		RG RIKEN Genome Exploration Research Group, and Genome Science Group
DE	clone:3310056B01 product:hypothetical protein	full insert sequence		(Genome Network Core Team) and the FANTOM Consortium;
DE	(10 days lactation adult female mammary gland cDNA)	RIKEN full-length enriched library, Clone:D70039103 product:hypothetical protein, full insert sequence)		RT RT "Antisense Transcriptome in the Mammalian Transcriptome.";
DE	enriched library, Clone:F330208E07 product:activated spleen cDNA	RIKEN full-length enriched library, Clone:FB330208E07 product:hypothetical protein, full insert sequence)		RL RN
GN	Name=21010318G18Rik;			[4] SCIENCE 309:1553-1563 (2005).
OS	Mus musculus (Mouse)			RP NUCLEOTIDE SEQUENCE.
OC	Chordata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Mammary gland,
OC	Mammalia; Eutheria; Euchondrocytes; Glires; Rodentia; Sciurognathi;			RC Tongue, and Whole body/
OC	Muroidea; Muridae; Murinae; Mus.			RC Tongue, and Whole body;
OX				RX RX
RN				PUBMED=12466851; DOI=10.1038/nature01266;
RP				Medline=22354683; PubMed=12466851;
RC				RA Okaishi Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RC				RA Tomaru Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RC				RA Okaishi Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RC				RA Okaishi Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RC				RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RC				RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RC				RA Schirimi L.M., Marchionni L., McKenzie L., Miki H.,
RC				RA Blake J.A., Bradt D.A., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RC				RA Dalla B., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RC				RA Gaasterland T., Garibaldi M., Gissi C., Godzik A., Gough J.,
RC				RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RC				RA Kanai A., Kawai H., Kawaseawa Y., Kedzierski R.M., King B.L.,
RC				RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RC				RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RC				RA Nagashim T., Numata K., Okido T., Pavani W.J., Peretea G., Pesole G.,
RC				RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RC				RA Ravasi T., Reid J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RC				RA Sandelin A., Schneider C., Semple C.A., Setou M., Shiota K.,
RC				RA Sultan A., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,
RC				RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RC				RA Wilming L.G., Wynnshaw-Boros A., Yanagisawa M., Yang I., Yang L.,
RC				RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RC				RA Hirao T., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RC				RA Hirao T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RC				RA Hara A., Hashizume W., Inotani K., Ishii Y., Itou M., Kagawa I.,
RC				RA Miyazaki A., Sakai K., Sasaki D., Shibaoka K., Shinagawa A.,
RC				RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RC				RA Birney B., Hayashizaki Y.;
RC				RT "Analysis of the mouse transcriptome based on functional annotation of
RC				RT 60,770 full-length cDNAs.";
RC				RL RN
RN				[5] NATURE 420:563-573 (2002).
RP				RP NUCLEOTIDE SEQUENCE.
RC				RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Mammary gland,
RC				RC Tongue, and Whole body/
RC				RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RC				RA Kawai J., Shinagawa T., Shibata K., Yoshino M., Ichii Y.,
RC				RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RC				RA Aizawa K., Izawa M., Nishi K., Kiyanuka I., Kondo S., Yamanaka I.,
RC				RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RC				RA Kadota K., Matsuda H., Batalov S., Casavant T.,
RC				RA Fleischmann W., Gaasterland T., Giessi C., King B., Kochiwa H.,
RC				RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RC				RA Schirimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RC				RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RC				RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RC				RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RC				RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RC				RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
RC				RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
OY	181	HSGNFGTDLQKHLWNPDKGTVLHMITTAEWMSFFGGFPFLTYIRDFQKISLRYEAN	240	Ueda H.R., van Nimwegen E., Verardo R., Wei C.I., Yagi K.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:655-659(2000). [6]

RNA NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; and NOD; TISSUE=Activated spleen, Mammary gland, Tongue, and whole body;
MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;

RNA Carrinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1611-1630 (2000). [7]

RNA NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Mammary gland, Tongue, and whole body;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RNA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., Konno H., Akiyama Y., Nakamura S., Hisamatsu M., Nishimura T., Harada A., Sumi N., Ishii Y., Nakamura S., Hisamatsu M., Nishimura T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchi M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kir A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771 (2000). [8]

RNA NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Tongue, and whole body;
Adachi J., Aizawa K., Akaihara S., Akimura T., Arai A., Aono H., Furuno M., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanegaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoaka T., Hori F., Imotani K., Ishii Y., Konno H., Itoh M., Izawa M., Kasukawa T., Kato T., Kawai J., Koijima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamuro T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases. [9]

RNA NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Mammary gland;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno H., Hanagaki T., Hara A., Hashizume W., Hayashida C., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kato H., Kawai J., Koijima Y., Kondo S., Kondo H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saito H., Sakai C., Sakai K., Shinagawa A., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Togawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases. [10]

RNA NUCLEOTIDE SEQUENCE.
STRAIN=NOD; TISSUE=Activated spleen;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Inamura K., Imotani K., Ichii M., Kanagawa S., Hori F., Length 267; Score 1245; DB 2; Pred. No. 1.1e-95; Mismatches 17; Indels 0; Gaps 89.4%; Best Local Similarity 86.4%; Matches 229; Conservative 19;

Query Match 1 MNWFOGLSEPSALVIVTSSAIFSYTTLHHDPAFLPYISDTGTVAPEKCLFGAML

Db	1	MWNQQGLSFLPSALVIVTPATFFSYTAITLHVDPALPYISDTGTIPPERCLFGVML
Qy	61	NIAAVLCLATIYVRYKQVHALSPPEVNVIKLNKAGLVGILSCLCLSLIVANFOKTTLFAA 124
Qy	61	NIAAVLGLATMRYKQVHALNPENLITKLNKAGLVGILSCLCLSLIVANFOKTTLFIV 124
Db	121	HVGCAVLTFCMGSIYMFQITLSQMQPKIHKGKOFENWIRLLVIVCGVSALSMSLTCSSVL 184
Db	121	HVGCAVLAFCMGSSYMFQITLSQMQPKIHKSQVFWRLLLWIVCGVSALSMSLTCSSVL 184
Qy	181	HSGNFGTDLDEQKLHNPDKGYVHMMITAENSMSFSFEGFFLTYIRDQKISLRVEAN 24
Db	181	YSSNFGPDVYQKLHNPDKGYVHMMITAENSMSFSFEGFFLTYIRDQKISLRVEAN 24
Qy	241	LHGTLTYDTPCAPCPINNERTPLSSRD 265
Db	241	LHGTLTYDTPCPINNERTPLSSRD 265
Qy	241	LHGTLTYDTPCPINNERTPLSSRD 265
RESULT 5		
	OSBK09 RAT	PRELIMINARY;
	ID QSBK09; RAT	PRP;
	AC QSBK09;	267 AA.
	DT 12-APR-2005,	integrated into UniProtKB/TREMBL.
	DT 07-FEB-2006,	sequence version 1.
	DB Hypothetical protein LOC362011.	entry version 7.
	GN Name=LOC362011;	
	OS Rattus norvegicus (Rat).	
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	OC Mammalia; Eutheria; Eucarchontoglires; Glires; Rodentia; Sciurognathi;	
	OC Muroidea; Muridae; Murinae; Rattus.	
	OX NCBI_TaxID=10116;	
	RN [1]	
	RP NUCLEOTIDE SEQUENCE.	
	RC TISSUE-Liver;	
	RX MEDLINE=2238817; PubMed=12477932; DOI=10.1073/pnas.222603899;	
	RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
	RA Klaunser R.D., Collins F.S., Wagner L., Schuler G.D.,	
	RA Alischul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F.,	
	RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
	RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
	RA Stapleton M., Sozae M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
	RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
	RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullhy S.J.,	
	RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratine P.H.,	
	RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
	RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
	RA Fahay J., Kettman M., Madan A., Rodriguez S., Sanchez A.,	
	RA Whiting M., Madan A., Young A.C.Y., Shevchenko Y., Bouffard G.G.,	
	RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
	RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
	RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,	
	RA Schniech A., Schein J.E., Jones S.J.M., Marras M.A.;	
	RT "Generation and initial analysis of more than 15,000 full-length human	
	RT and mouse cDNA sequences";	
	RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
	RN [2]	
	RP NUCLEOTIDE SEQUENCE.	
	RC TISSUE-Liver;	
	RG NIH MGIC Project;	
	RL Submitted (MAR 2005) to the EMBL/GenBank/DDBJ databases.	
--	--	
CC	Copyright by the UniProt Consortium, see http://www.uniprot.org/terms	
CC	Distributed under the Creative Commons Attribution-NonDerivs License	
CC		
DR	BC091251; AAH91251.1; - mRNA.	
KW HYPOTHETICAL PROTEIN.		
SQ SEQUENCE 267 AA; 30173 MW; 5B8D99C7A8B018E1 CRC64;		
Query Match 88.8%; Score 1236; DB 2; Length 267;		
Best Local Similarity 86.0%; Pred. No. 6.4e-55;		
March 22, 2006. Conservative 18. Misaligned 19. Index 0; Gap 0		

Qy 1 MWIFQQGSLPLPSALVINTSAAPITFSYTTAVTLHIDPALPYISDTGGVAPERKCLFGAML 60
 DB 1 MWIFQQGSLPLPSALVINTFATFSTYTTAVTLHVDALPISDTGGMPPERCLFGVML 60

Qy 61 NIAAVLCAITIYRYKQVHALSPBENVTLKLNAKLGLSLSLTSVANFOKTTLFAA 120
 DB 61 NIAAVLGAITIYRYKQVHALNPBNLTLKLNAKLGLSLSLTSVANFOKSALFIV 120

Qy 121 HVCGAVLTFGMGSLSYMFYOTILSYQMQKIHGQVENVRLIIVCGVSALSMLTCSVLI 180
 DB 121 HVCGAVLFSMGSFYMFYOTILSYQMQKIHSGKQVENVRLIIVCGVSALSMTCSSIL 180

Qy 181 HSGNFGTDLQKQHWNPDKGTVLHMITTAEKSMSMSPFFGFLTYIRDFOKITLVEAN 240
 DB 181 YSSDFGAIVQKLHWNPDKGTVLHMITTAEKSMSMSPFFGFLTYIRDFOKITLVEAN 240

Qy 241 LHGLTLYDTPACPINNERTLISRD 265
 DB 241 LHGLTLYDTPCPVPTNERPLLSRD 265

RESULT 6

Q9D520_MOUSE PRELIMINARY; ERT; 267 AA.
 ID Q9D520_MOUSE PRELIMINARY; ERT; 267 AA.
 AC D01-JUN-2001, integrated into UniProtKB/TREMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DE Adult male testis cDNA, RIKEN full-length enriched library,
 clone #A30524M19 product: RIKEN cDNA 2610318G18
 DE Name=2610318G18Rk;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchoontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN RP

NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Testis;
 RXN MEDLINE=9929253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RA RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 03:19-44 (1999).
 [2]

RP

NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Testis;
 RXN MEDLINE=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodaius R., Shimokawa K.,
 RA Baiji V.B., Bremer S.B., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Banski J., Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Baxter L., Beisel K.W., Barsano T., Bono H., Chalk A.M.,
 RA Chiu P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalziel B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 RA Fletcher C.P., Fukushima T., Furuno M., Garibaldi M.,
 RA Georgiou-Hemming S., Gingera T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminiecki L., Iacono M., Itoe K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarev D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Muider N., Nakano N., Nauchka H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavani W.J., Pavesi G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ringwald M.,
 RA Reuter B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Setiguchi K., Simple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,

RA Sperling S., Stupka E., Sugiura K., Sultan R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang R., Taylor J., Teichmann S.A.,
 RA Teda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamamoto H., Zabarovsky B., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu B.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Rume D.A., Kai C., Sasaki D.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura T., Kojima M., Kato T., Kawahashi N.,
 RA Kawashima T., Okada M., Plesey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanuki A., Okamura-Ohno Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).
 [3]

RN RP

NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RXN MEDLINE=22354682; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamakata I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hassegawa Y., Nagami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,
 RA Dalla B., Dragani T.A., Fletcher C., Forrest A., Frazer K.S.,
 RA Gaasterland T., Garibaldi M., Gissi C., Godzik A., Gough J., Jarvis E.D.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackman I.J., Jarvis E.D.,
 RA Kania A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavani W.J., Peretea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Raveasi T., Reed J.C., Reid D.J., Reid J., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Tonita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasada D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 [5]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RXN MEDLINE=21085660; PubMed=11212851; DOI=10.1038/35055500;
 RA Kawai J., Shinadawa A., Shibata K., Yoshino M., Ichii M., Ishii Y.,
 RA Hill D., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saico R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Purino M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Bofelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Monbaerts P.,
 RA Nordone P., Ring B., Ringwald M., Ringwald M.,
 RA Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynn-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL *Nature* 409:685-690 (2001).
 RN [16]
 RP NUCLEOTIDE SEQUENCE /PR: STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL *Genome Res.* 10:1617-1630 (2000).
 RN [17]
 RP NUCLEOTIDE SEQUENCE /PR: STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=0530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Carninci P., Itoh M., Aizawa K., Nagano M., Niishina M., Nishimura S.,
 RA Konno H., Akiyama J., Nishii K., Kitamura T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazana M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuri S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kiria A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system: 384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL *Genome Res.* 10:1757-1771 (2000).
 RN [18]
 RP NUCLEOTIDE SEQUENCE /PR: STRAIN=C57BL/6J; TISSUE=Testis;
 RC Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagata N., Hara A., Hayatsu N., Hirayama T., Hirata K.,
 RA Imotsiki T., Hara T., Itoh M., Kasukawa T., Kato H.,
 RA Imotsiki T., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sobage Y., Suzuki H., Tagami M., Tagami T., Tagami Y., Tanaka T.,
 RA Teijima Y., Toyoda T., Yamagata T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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 DR EMBL: KR015888; BAB300020_1; mRNA.
 DR Ensembl: ENSMUSG0000027900; Mus musculus.
 DR MGII: MGII:1914421; 2610318GB1RICK.
 SQ SEQUENCE 267 AA; 30244 NW; 228214D5AFF37CEP CRC64;
 Query Match 88.7%; Score 1235; DB 2; Length 267;
 Best Local Similarity 86.0%; Pred. No. 7, 8e-95;
 Matches 228; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
 1 MWNFQGGSFLPSALVITSAAFPSYTAATLHIDALPYTSDTGVAPEKCLFGML 60
 1 MWNFQGGSFLPSALVITPAFIFSYTTAITHVDAALPYTSDGTPPERCLFGML 60
 QY 61 NIAAVLCAATIYRYKQVHALSPPEENVIKLKAGLVGILSCLGLSVANFOKTTLFAA 120
 db 61 NIAAVLCAATIYRYKQVHALNPENLTIKLNAGLVGILSCLGLSVANFOKTTLFAA 120
 QY 121 HVSGAVLTFGMGSLYMFVQTLISYQMQPKHQVKQVFLRLVWCGVSALEMTCSSVL 180
 db 121 HVSGAVLTFGMGSLYMFVQTLISYQMQPKHQVKQVFLRLVWCGVSALEMTCSSVL 180
 QY 181 HSGAVLTFGDGVVQKLVHNPDKGYVHLVTAEMSMSFFGGFLTYIRDFOKITLVEAN 240
 db 181 YSSDFGPDVQKLVHNPDKGYVHLVTAEMSMSFFGGFLTYIRDFOKITLVEAN 240
 Qy 241 LHGLTLYDTAPCPINNERTLLSRD 265
 Db 241 LHGLTLYDTCPCLVNERTPLSLRD 265

RESULT 7
 Q9D835_MOUSE PRELIMINARY; PRT; 180 AA.
 ID Q9D835_MOUSE
 AC Q9D835_
 DT 01-JUN-2001, integrated into UniProtKB/TREMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 01-FEB-2005, entry version 22.
 DE Adult male small intestine cDNA, RIKEN full-length enriched library,
 clone:201030514 product:RIKEN cDNA 201030514 (Hypothetical protein
 DE Tmem77).
 GN Name=2610318GB1RICK; Synonyms=Tmem77;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 RN [1]
 RP Nucleotide Sequence /PR: STRAIN=C57BL/6J; TISSUE=Small intestine;
 RN Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Okama R., Ravasi T., Lenhard B., Wells C., Rodzis R., Shinomura K.,
 RA Bajic B., Bremer S.E., Batyalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aiden L.E.,
 RA Ambesi-Impiombato A., Apweiler R., Aturalioglu A.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Choi K.P., Choudhury V., Christoforidis A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Garibaldi M.,
 RA Georgini-Hemming P., Gingras T.R., Gojobori T., Green R.E.,
 RA Georginich S., Harbors M., Hayashi Y., Hensel T.K., Hirokawa N.,
 RA Hill D., Humblet L., Iacono M., Ieko K., Iwama A., Ishikawa T.,
 RA Jak M., Kanapin A., Katoch M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollidas G., Krishnan P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarovic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam H., Madan Babu M., Madara S., Marchionni L.,
 RA Matushita H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavani W.J., Pavesi G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Ros B., Ruan Y., Schmid B., Sandelin A., Schneider A.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sesha L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silvia D., Sinclair B.,
 RA Sperling E., Stupka Y., Sugiyura K., Suliana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegnér J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamamoto H., Zabarsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmer S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Takayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plesey C., Shiribata K., Suzuki S.,
 RA Tagami M., Wakai K., Watshiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).
 RN [13]
 NUCLEOTIDE SEQUENCE

Qy	121	HVSAGAVLITFGMGSLYMFVQTILSYQMQPKIHKGKQFWIRLLIVWCGSALSMLTCSSVL	180	Db	1	MWWFFEGGLCVLPVALVVWTAATFIPAYITAVVLRHVDPLVPIISDTGTVAPERCVFGYML	60
Db	114	-----	113	Qy	61	NIAAWUCLATIIVYVKVHALSP_FENVIKLINKAKGLVIGLISCUGLSIVANFOKTTLPA	119
Db	114	-----	114	Db	61	NVSAFLGVATMYVKQQLADYDDTRANRLNFGVFCGCSSEGMCCVANFORTLPS	120
Qy	181	HSGNFGTIDLEQKLHWNPDKGYVLNMTAAEWSMSFFGKQFQKISLVEAN	240	Qy	120	AHVSSAVLIFGMSLYMFVQTILSYQMQPKIHKGKQFWIRLLIVWCGSALSMLTCSSV	179
Db	114	-----	153	Db	121	MHLVGAIIIEFGKQFQKISLVEAN	180
Qy	241	LHGGLTYDTPCPINNESTRLLSRD	265	Qy	180	LHSGNFGTIDLEQKLHWNPDKGYVLHMITAAEWSMSFFGFLTYIRDFOKISLVEA	239
Db	154	LHGGLTYDTPCPINNESTRLLSRD	178	Db	181	MYSTPGEVTKKLHWTGPBGPFTAHIVSTISENSLALSFISFFTYIRDDEKKINLRASA	240
RESULT 8							
QEIQIO_BRAKE	PRELIMINARY;	PRT;	272 AA.	Qy	240	NLHGHTLYDT	249
ID	QEIQIO_BRAKE	PRELIMINARY;	PRT;	Db	241	ELQSNHLYES	250
AC							
DR	05-JUL-2004	integrated into UniProtKB/TREMBL.					
DT	05-JUL-2004	sequence version 1.					
DT	07-FEB-2006	entry version 13.					
DE	Hypothetical protein zgc:86754.						
CN	ORFName=zgc:86754;						
CS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.						
OC	NCBI_TAXID=7955;						
OX							
RN							
RC	NUCLEOTIDE SEQUENCE.						
RX	TISSUE=Embryo;						
RX	MEDLINEB-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;						
RA	Straussberg R.D., Peingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeisberg B., Buetow K.H., Schaefer C.F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toohinity S., Carrinco P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullany S.J., Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heilton B., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Snailus D.E., Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).						
RN	[2]	NUCLEOTIDE SEQUENCE.					
RP	TISSUE=Embryo;						
RC	NIH MGIC Project;						
RG	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.						
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CC	Distributed under the Creative Commons Attribution-NoDerivs License						
CC							
DR	EMBL; BC071426; AAH71426.1; mRNA.						
DR	ZFIN; ZDB-GENE-040625-141; zgc:86754.						
KW	Hypothetical protein.						
SQ	SEQUENCE 272 AA;						
Query Match	54.9% ; Score 764.5 ; DB 2 ; Length 272 ;						
Best Local Similarity	55.2% ; Pred. No. 1..6-55 ; Indels 1 ; Gaps 1 ;						
Matches	138 ; Conservative 48 ; Mismatches 63 ;						
RESULT 10	1 MWWFOGLSPFLPSALWVTSAAFIFSYIATVTLHIDPAPLYISDTGTVAPEKLGFGML	60					
Qy	1 MWWFOGLSPFLPSALWVTSAAFIFSYIATVTLHIDPAPLYISDTGTVAPEKLGFGML	60					
ID	QB6682_HUMAN						
QB6682;	QB6682;						
Db	121 PCPINNERTLLSRDI	136					

DR	01-OCT-2002, integrated into UniProtKB/TREMBL.	Q9DC58_MOUSE	PRELIMINARY;	PRT;	238 AA.
DT	01-OCT-2006, sequence version 1.	ID Q9DC58_	AC	DT 01-JUN-2001, integrated into UniProtKB/TREMBL.	.
DE	FLJ11259 protein.	DT 05-JULY-2004, sequence version 16.	DT 05-JULY-2004, sequence version 16.	DT 05-JULY-2004, sequence version 16.	.
GN	Name=FLJ11259;	DT 07-FEB-2006, entry version 20.	DT 07-FEB-2006, entry version 20.	DT 07-FEB-2006, entry version 20.	.
OS	Homo sapiens (Human).	DE Adult male lung cDNA, RIKEN full-length enriched library, clone:1200002N14 product hypothetical RNA-banding region RNP-1 (RNA recognition motif) containing protein, full insert sequence.	DE DE	DE DE	DE DE
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo; Butheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.	GN Name=120002N14rik;	OS Mus musculus (Mouse)	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.	OC OC
OC	NCBI_TAXID=9606;	OX NCB TaxID=10090;	OX RN	OX RN	OX RN
RN	RP NUCLEOTIDE SEQUENCE.	RC NUCLEOTIDE SEQUENCE.	RC NUCLEOTIDE SEQUENCE.	RC NUCLEOTIDE SEQUENCE.	RC NUCLEOTIDE SEQUENCE.
RC	TISSUE=Liver;	RA STRAIN=C57BL/6J; TISSUE=Lung;	RA STRAIN=C57BL/6J; TISSUE=Lung;	RA STRAIN=C57BL/6J; TISSUE=Lung;	RA STRAIN=C57BL/6J; TISSUE=Lung;
RX	MDLNAME=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;	RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altenschul S.F., Zeeberg B., Buetow K.H., Bhat N.K., Atkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heihs F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J., Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Tsohuvski S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muñoz D.M., Sodergren B.J., Lu X., Gibbs R.A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialus D.E., Schnurch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Bremer S.E., Batzalos S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Berbano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dairymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Garibaldi M., Georgii-Hemmings P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jak T.M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitanoto H., Kollrias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazaravic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Miyrone F., Miyake S., Morris K., Motaguchi-Tarab S., Mulder N., Nakano N., Nakuchi H., Ng P., Nilsson R., Nishizuchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang W.J., Pavani P.C., Pesole G., Petrovsky N., Piazza S., Reed J.J., Reid J.F., Ringwald M., Rost B., Ruan Y., Sandelin A., Schneider C., Shiba T., Shibusawa Y., Shimada H., Shimada K., Siliva D., Sinclair B., Sperling S., Stropula E., Sugiyura K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen B., Verardo R., Wei C.L., Yagi K., Yamamoto H., Zabarsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmelund S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Rada-Iglesias A., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Niishio T., Okada M., Plesey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watanuki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y., "The transcriptome landscape of the mammalian genome.";	RA RN	RA RN	RA RN
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- [4] NUCLEOTIDE SEQUENCE.
STRAIN=C5BL/6J; TISSUE=Lung;
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Nakada I., Oiso N., Saico R., Suzuki H., Yamana K. I., Kiyosawa H.,
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Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
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STRAIN=C5BL/6J; TISSUE=Lung;
RC PubMed=10530913; PubMed=11076861; DOI=10.1101/gr.126000;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
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- RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujikawa S., Inoue Y., Togawa M., Iizawa M., Ohara E., Watabiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuuwa S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RISA integrated sequence analysis (RISA) system-384 format
sequencing pipeline with 384 multicapillary sequencer." RTR
Genome Res. 10:1757-1771 (2000).
RN [8].
- NUCLEOTIDE SEQUENCE.
STRAIN=C5BL/6J; TISSUE=Lung;
RC Akimura T., Arai A., Aono H., Arai J., Aizawa K., Akihara S.,
Arakawa T., Bono H., Carninci P., Fukuda S., Furukoshi Y., Furuno M.,
Hanageki T., Hara A., Hayatsu N., Hiramoto K., Hirayama T., Hori F.,
Imotani K., Itoh Y., Itoh M., Kasukawa T., Kato H.,
Kawai J., Koijima Y., Kono H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa R., Saito H., Saito K., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shiraki T., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshihino M.,
Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
- RA Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
- RA DR AK004552; BAB23366.2; -; mRNA.
DR Ensembl; ENSMUSG00000020057; Mus musculus.
DR MG1:1918962; 120002N14rik.
DR GO:0003676; F:nucleic acid binding; RCA.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26201 MW; AC89F1301B0A0048 CRC64;
- Query Match 34 4%; Score 479 5%; DB 2; Length 238;
Best Local Similarity 37.3%; Pred No. 8.5e-32; Indels 21; Gaps 3;
Matches 93; Conservative 56; Mismatches 79; Indels 21; Gaps 3;
- Qy 1 MWAFQQLSPPSALVWTSAAPIFSYITAVTLHHDPALPYISDTGTVAPEKCFQGAML 60
Db 1 MLCLFRGMAYFVFLIVTWSSAFAISYVWAVLSGHVNPFPLYISDTGTTPESGIGFM 60
Qy 61 NIAAVIACIATYVRRQV-----HALSPBPENVIKLNAKLGVILGILSCGLSVANFQ 113
Db 61 NFSAFGLGAATNYTRKIVEKONETCYFSTPYPENLU-----SLALGLVGCTGMGIYANFQ 114
Qy 114 KTTLFIAAHVSGAVLITGMGSYIMFVOTILSYQMPKIRGKOVFWRLLTWCGVSALSM 173
Db 115 EIAVPVHDGALLAFVGVVYTLISIYSKSCPWNLSLTCHYMAISAVSCAAVPM 174
Qy 174 LTCSSVLHSGNFGTDLQKLNHNPEDKGKVYLHMITTAEMMSFSFFGPFLTYIRDQKI 233
Db 175 IACASLTSI-----TKLWNPKERDYIYHVAACENTVAGFIFYFLTFIDFQS 226
DE 29c:101:111.
GN ORFNames=zgc:101811; Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RA [1]

RP	NUCLEOTIDE SEQUENCE; TISSUE=Olfactory epithelium;	OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
RX	MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;	OC	Cyprinidae; Danio.
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	OX	NCBITaxID=955;
RA	Klausner R.D., Collins F.S., Wagner L., Shneifer C.M., Schuler G.D.,	[1]	RN
RA	Aalschuij S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	RP	NUCLEOTIDE SEQUENCE.
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	RA	Clark S.;
RA	Dichtshenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,	RL	Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carriuci P., Scheetz T.E.,	CC	Distributed under the Creative Commons Attribution-NoDerivs License
RA	Raha S.S., Loquellano P.N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	DR	CC
RA	Botak S.A., McEwan P.D., Mckernan K.J., Malek J.A., Gunaratne P.H.,	DR	EMBL; BX890572; CAI11845_1; - Genomic DNA.
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	DR	Ensembl; ENSDARG00000045561; Danio rerio.
RA	Villanueva D.K., Munay D.M., Sodergren E.J., Lu X., Gibbs R.A.,	ZFIN; ZDB-GENE-041010-147; zgc:101811.	
RA	Fahey J., Heiton B., Ketteman M., Madan A., Rodriguez S., Sanchez A.,	SO	SEQUENCE 240 AA; 27112 MW; 4A50CE57BA2F24D7 CRC64;
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	Query Match	34.2%; Score 476.5; DB 2; Length 240;
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,	Best Local Similarity	39.7%; Pred. No. 1.5e-51;
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	Matches	96; Conservative 43; Mismatches 94; Indels 9; Gaps 3;
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	Db	1 MWFFQGQISFLPSALVIWTSAAFIFSYTAVTLHHIDPALPYISDTGVAPERKCLFGAML 60
RA	Schnierch A., Schein A., Jones S.J.M., Marra M.A.,	Db	1 MWFMEGMICFLPTFLVTSSTPIISYIALYRQDVWLPISDTGPBESCVFGFMS 60
RR	"Generation and initial analysis of more than 15,000 full-length human	Qy	61 NIAAVLCAIATYVRYKQHALSPEENVI-IKLINKAGLVLGISLIVANFQKTTLFA 119
RR	and mouse cDNA sequences.";	Qy	61 TTTAAFAATMYAAYKFVERVHRTGAPPTPLNKVSFGFGFSCIGCLVATQETTVME 120
RR	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	Db	61 AHVSGAVLTFGMGSYMFQQTLSYOMQPKIHKGKQVFWRILLVIVCGVSALSMLTCSSV 179
RN	NUCLEOTIDE SEQUENCE; TISSUE=Olfactory epithelium;	Qy	120 VHDIGALFFIGCVYAVIQSVIGTRAFFYQGSSSKFENCHLRTFFSTVAILAAIPTIACGFL 180
RN	director MGC Project;	Db	121 VHDIGALFFIGCVYAVIQSVIGTRAFFYQGSSSKFENCHLRTFFSTVAILAAIPTIACGFL 180
RN	Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.	Db	180 LHSGNFGSTDLEQKLHNPNPDKGYVILIMITTAEWSMSFSFGFELTYIRDFOKISIRVEA 239
RN	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	Qy	181 V----GT---SKLHWDSNDKDVTHTIVSVACEWITIFSUVFFFTLYIQEFQQTFLKLTV 232
RN	Distributed under the Creative Commons Attribution-NoDerivs License	Db	240 NL 241
RN	EMBL; BC083290; AAH83290.1; - mRNA.	Qy	240 NL 241
RN	Ensembl; ENSDARG0000045561; Danio rerio.	Db	233 NL 234
RN	SEQUENCE 240 AA; 27064 MW;	RESULT 14	XENTR
RN	5B40DP478A328E60 CRC64;	ID	Q5EAK8_XENTR
RN	Query Match	ID	Q5EAK8_XENTR
RN	34.3%; Score 477.5; DB 2; Length 240;	AC	PRELIMINARY; PRT; 239 AA.
RN	Best Local Similarity	AC	PRELIMINARY; PRT; 239 AA.
RN	39.7%; Pred. No. 1.3e-31;	DE	integrated into UniProtKB/TREMBL.
RN	Mismatches 94; Indels 9; Gaps 3;	DE	DT 15-MAR-2005, integrated into UniProtKB/TREMBL.
RN	Db	DE	DT 15-MAR-2005, sequence version 1.
RN	1 MWFFQGQISFLPSALVIWTSAAFIFSYTAVTLHHIDPALPYISDTGVAPERKCLFGAML 60	OS	DT 07-FEB-2005, entry version 7.
RN	1 MWFMEGMICFLPTFLVTSSTPIISYIALYRQDVWLPISDTGPBESCVFGFMS 60	OS	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
RN	61 NIAAVLCAIATYVRYKQHALSPEENVI-IKLINKAGLVLGISLIVANFQKTTLFA 119	RA	OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN	61 TTTAAFAATMYAAYKFVERVHRTGAPPTPLNKVSFGFGFSCIGCLVATQETTVME 120	RA	OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
RN	120 AHVSGAVLTFGMGSYMFQQTLSYOMQPKIHKGKQVFWRILLVIVCGVSALSMLTCSSV 179	RA	OC Xenopoda; Xenopus; Silurana.
RN	121 VHDIGALFFIGCVYAVIQSVIGTRAFFYQGSSSKFENCHLRTFFSTVAILAAIPTIACGFL 180	RA	NCBIPrimaryID=8364; XENTR
RN	180 LHSGNFGSTDLEQKLHNPNPDKGYVILIMITTAEWSMSFSFGFELTYIRDFOKISIRVEA 239	RA	NCBI_TaxID=955; NUCLEOTIDE SEQUENCE.
RN	181 V----GT---SKLHWDSNDKDVTHTIVSVACEWITIFSUVFFFTLYIQEFQQTFLKLTV 232	RA	RC TISSUE=Whole body; RC MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RN	240 NL 241	RA	RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Brachydanio rerio (Zebrafish) (Danio rerio). Bokulich N.A., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA	Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schein A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E., Schein A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RA	TISSUE=Whole body;	RA	NUCLEOTIDE SEQUENCE.
RA	Klein S., Gerhard D.S.; Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.	RP	NUCLEOTIDE SEQUENCE.
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	RC	TISSUE=Liver;
CC	Distributed under the Creative Commons Attribution-NoDerivs License	RX	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
CC	DR EBO90386; AAH90386; mRNA.	RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus Initiative"; RT Dev. Dyn. 225:384-391 (2002).
SQ	SEQUENCE 239 AA; 26578 MW; 25040C8CB4A34DA8 CRC64;	RL	RT Initiated (MAY 2004) to the EMBL/GenBank/DDBJ databases.
Query	Query Match 34.0%; Score 473.5; DB 2; Length 239; Best Local Similarity 39.4%; Pred. No. 2.7e-31; Matches 95; Conservative 55; Mismatches 82; Indels 9; Gaps 4;	RA	RA Klein S., Strausberg R.; RC TISSUE=Liver; RL Submitted (MAY 2004) to the EMBL/GenBank/DDBJ databases.
Db	3 WFOQGLSFLPSALVWTSAAFISYTTAVTLRHHIDPAPYISDTGTVAPEKCLFGAMLN 62	CC	CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Db	4 WCLHGAAALPLSPSILVWSAGFLFSYIISVLIGHVPPPPYISDTGTSPPESGVFGMISL 63	CC	CC Distributed under the Creative Commons Attribution-NoDerivs License
Db	53 AVVICIATIIVRYRKQVHALSPEENVIT-IKLANKAGLVIGLISLSCUGLSIVANFOKTTLFAAH 121	DR	CC DR EMBL: BC070646; AAA70646.1; -; mRNA.
Db	64 SAMIGGAATMYTRKILEQNHSTDFLPYFNKTSLAIGLLCGIGMGTAVTPEMAVPAH 123	FT	FT NON_TER 1 1
Db	122 VSGAVLTGPMGLYMFQVQILSYQMKPQIKHGVFWIRLILVWCGVYSAALSMTCSSVLH 181	SEQUENCE	FT NON_TER 1 1 MW; 5E9814FA488BB462 CRC64
Db	124 DAGLITPTCGVTVYLISQYISVKSCPWNTRCHRMASVTAFTAVPM-SVFSVL- 181	Query	Query Match 33.9%; Score 471.5; DB 2; Length 287; Best Local Similarity 38.0%; Pred. No. 4.8e-31; Matches 93; Conservative 56; Mismatches 79; Indels 17; Gaps 4;
Db	182 SGNFGTDLQEQKLUHNPERDKGYHLMITTAENSMSFSSFGFFTYIRDFOKISLRVEANL 241	Db	3 WFOQGLSFLPSALVWTSAAFISYTTAVTLRHHIDPAPYISDTGTVAPEKCLFGAMLN 62
Db	182 SG----RKRLDWKPSDDEGHYHTLTAICENIVARGFMNFELTFIRDFOGVSQISTEI 235	Db	52 WCLQGAFLPLIVWSSAGFLPSYTISVLIGHVPPFPVPTISDRTSPPSGVFGMISV 111
Db	242 H 242	Db	63 AAVLCIATIIVRYRKQVHALSPEENVITK----MILERQNISIDFLPIYFNKISLAIGLFCIGMGIVATQEMAV 167
Db	236 H 236	Db	112 SAMLGATMTYR----MILERQNISIDFLPIYFNKISLAIGLFCIGMGIVATQEMAV 167
Result	RESULT 15	Db	118 FAAHVSQAVLTGPMGLYMFQVQILSYQMKPQIKHGVFWIRLILVWCGVYSAALSMTCSSVLH 177
ID	Q6NRS6_XENLA PRELIMINARY ; PRT; 287 AA.	Db	168 PAVHDAGALITIGQWVILLQSYISYKSCPTWNATCHIHMVSLIAFIAVPMVSFV 227
AC	Q6NRS6_	Qy	3 WFQQGLSFLPSALVWTSAAFISYTTAVTLRHHIDPAPYISDTGTVAPEKCLFGAMLN 62
DT	05-JUL-2004, integrated into UniProtKB/TREMBL.	Db	52 WCLQGAFLPLIVWSSAGFLPSYTISVLIGHVPPFPVPTISDRTSPPSGVFGMISV 111
DT	05-JUL-2004, sequence version 1.	Qy	63 AAVLCIATIIVRYRKQVHALSPEENVITK----MILERQNISIDFLPIYFNKISLAIGLFCIGMGIVATQEMAV 167
DT	07-FEB-2006, entry version 10.	Db	112 SAMLGATMTYR----MILERQNISIDFLPIYFNKISLAIGLFCIGMGIVATQEMAV 167
DE	LOC311986 protein (fragment).	Qy	118 FAAHVSQAVLTGPMGLYMFQVQILSYQMKPQIKHGVFWIRLILVWCGVYSAALSMTCSSVLH 177
CN	Name=Loc431986;	Db	168 PAVHDAGALITIGQWVILLQSYISYKSCPTWNATCHIHMVSLIAFIAVPMVSFV 227
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopoda; Xenopidae; Xenopus; Xenopus.	Qy	178 SVLHSGNFGTDLQEQKLUHNPERDKGYHLMITTAENSMSFSSFGFFTYIRDFOKISLRV 237
OC	Xenopidae; Xenopidae; Xenopus; Xenopus.	Db	228 --ILSG----RKRLDWKPSDDEGHYHTLTAICENIVARGFMNFELTFIRDFOGVSQI 279
OX	NCBI_TaxID=8355;	Qy	238 EANLH 242
RN	NUCLEOTIDE SEQUENCE.	Db	280 STEIH 284
RC	TISSUE=Liver;	Job time : 361 secs	Search completed: August 28, 2006, 17:37:33
RA	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Bhat N.K., Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		